



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:24 PM UTC

PDB ID : 7WOT / pdb_00007wot
EMDB ID : EMD-32658
Title : Cryo-EM structure of the inner ring monomer of the *Saccharomyces cerevisiae* nuclear pore complex
Authors : Li, Z.Q.; Chen, S.J.B.; Zhao, L.; Sui, S.F.
Deposited on : 2022-01-22
Resolution : 3.73 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

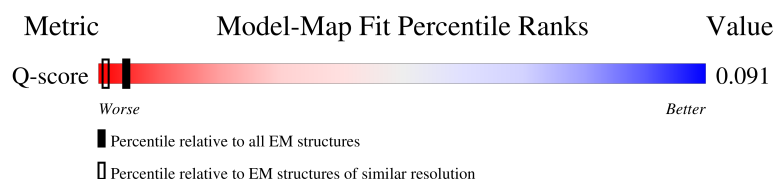
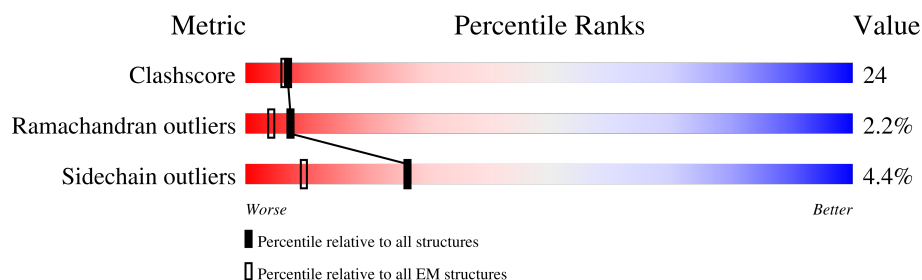
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.73 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10415 (3.23 - 4.23)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	839	78% 53% 32% • 13%
1	M	839	79% 52% 33% • 13%
1	N	839	29% 50% 31% 6% • 11%
1	Z	839	29% 51% 30% 6% • 11%

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Mol	Chain	Length	Quality of chain
2	C	1391	
2	O	1391	
3	D	1502	
3	P	1502	
4	E	1655	
4	Q	1655	
5	F	1683	
5	R	1683	
6	G	472	
6	J	472	
6	S	472	
6	V	472	
7	H	541	
7	K	541	
7	T	541	
7	W	541	
8	I	823	
8	L	823	
8	U	823	
8	X	823	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 133827 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Nucleoporin NIC96.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	732	Total	C	N	O	S	0	0
			5720	3628	975	1101	16		
1	M	729	Total	C	N	O	S	0	0
			5697	3616	972	1093	16		
1	N	746	Total	C	N	O	S	0	0
			5766	3656	976	1119	15		
1	Z	746	Total	C	N	O	S	0	0
			5767	3658	976	1118	15		

- Molecule 2 is a protein called Nucleoporin NUP157.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1325	Total	C	N	O	S	0	0
			10452	6664	1736	2018	34		
2	O	1325	Total	C	N	O	S	0	0
			10452	6664	1736	2018	34		

- Molecule 3 is a protein called Nucleoporin NUP170.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1398	Total	C	N	O	S	0	0
			10966	7012	1811	2111	32		
3	P	1398	Total	C	N	O	S	0	0
			10956	7005	1811	2108	32		

- Molecule 4 is a protein called Nucleoporin NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	1552	Total	C	N	O	S	0	0
			12362	8017	1981	2337	27		
4	Q	1552	Total	C	N	O	S	0	0
			12362	8017	1981	2337	27		

- Molecule 5 is a protein called Nucleoporin NUP192.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	1622	Total	C	N	O	S	0	0
			12239	7813	2031	2364	31		
5	R	1622	Total	C	N	O	S	0	0
			12239	7813	2031	2364	31		

- Molecule 6 is a protein called Nucleoporin NUP49/NSP49.

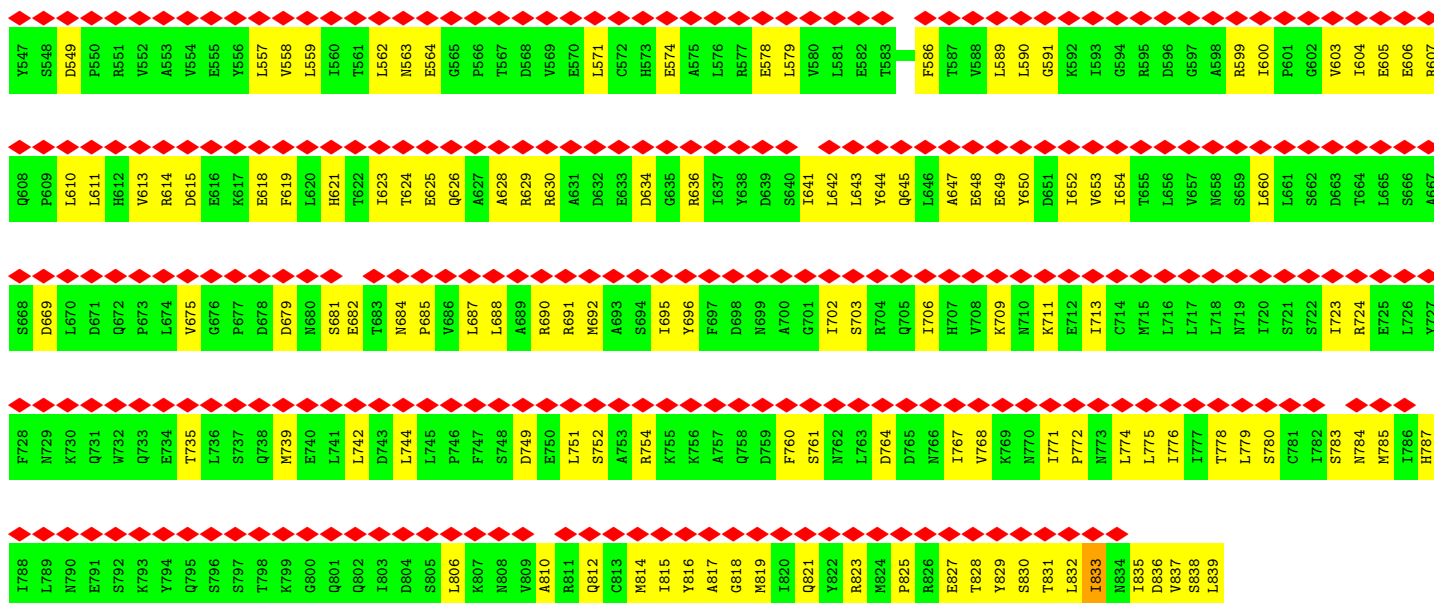
Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	200	Total	C	N	O	S	0	0
			1533	973	251	307	2		
6	J	195	Total	C	N	O	S	0	0
			1492	938	251	302	1		
6	S	200	Total	C	N	O	S	0	0
			1529	970	250	307	2		
6	V	195	Total	C	N	O	S	0	0
			1492	938	251	302	1		

- Molecule 7 is a protein called Nucleoporin NUP57.

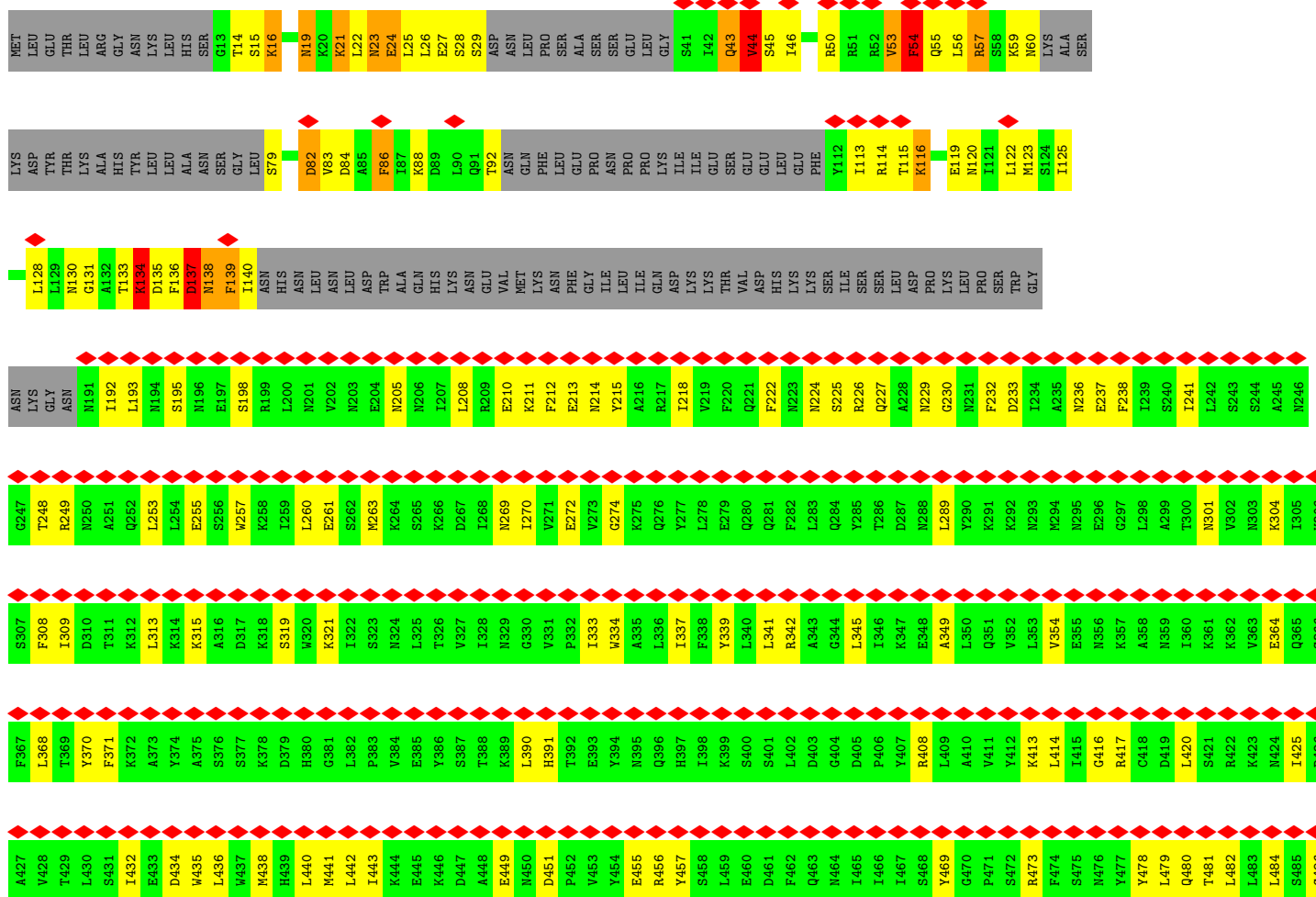
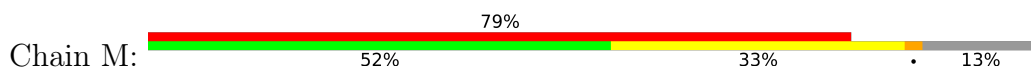
Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	246	Total	C	N	O	S	0	0
			1811	1128	332	348	3		
7	K	254	Total	C	N	O	S	0	0
			1808	1126	334	345	3		
7	T	246	Total	C	N	O	S	0	0
			1811	1128	332	348	3		
7	W	254	Total	C	N	O	S	0	0
			1805	1123	334	345	3		

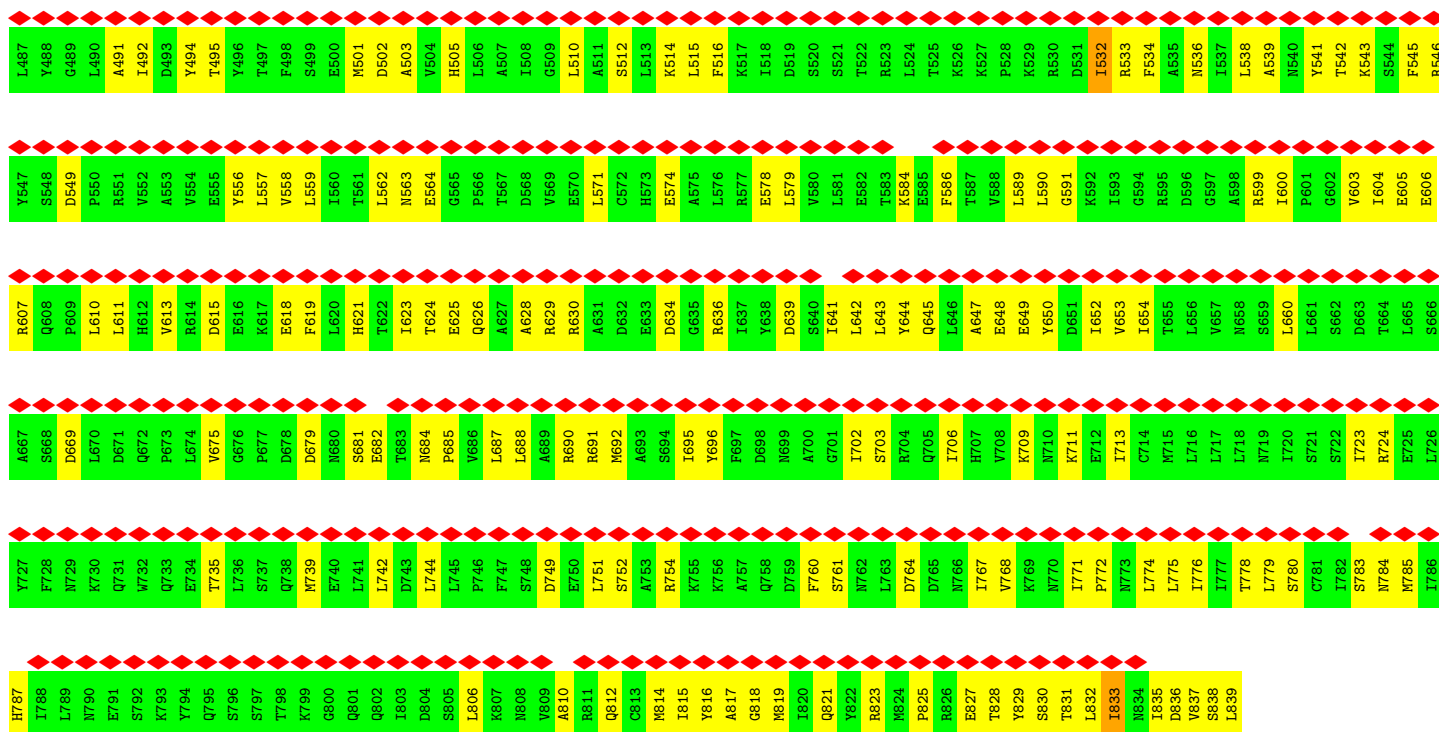
- Molecule 8 is a protein called Nucleoporin NSP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	187	Total	C	N	O	S	0	0
			1418	862	244	311	1		
8	L	187	Total	C	N	O	S	0	0
			1366	830	240	295	1		
8	U	187	Total	C	N	O	S	0	0
			1418	862	244	311	1		
8	X	187	Total	C	N	O	S	0	0
			1366	830	240	295	1		

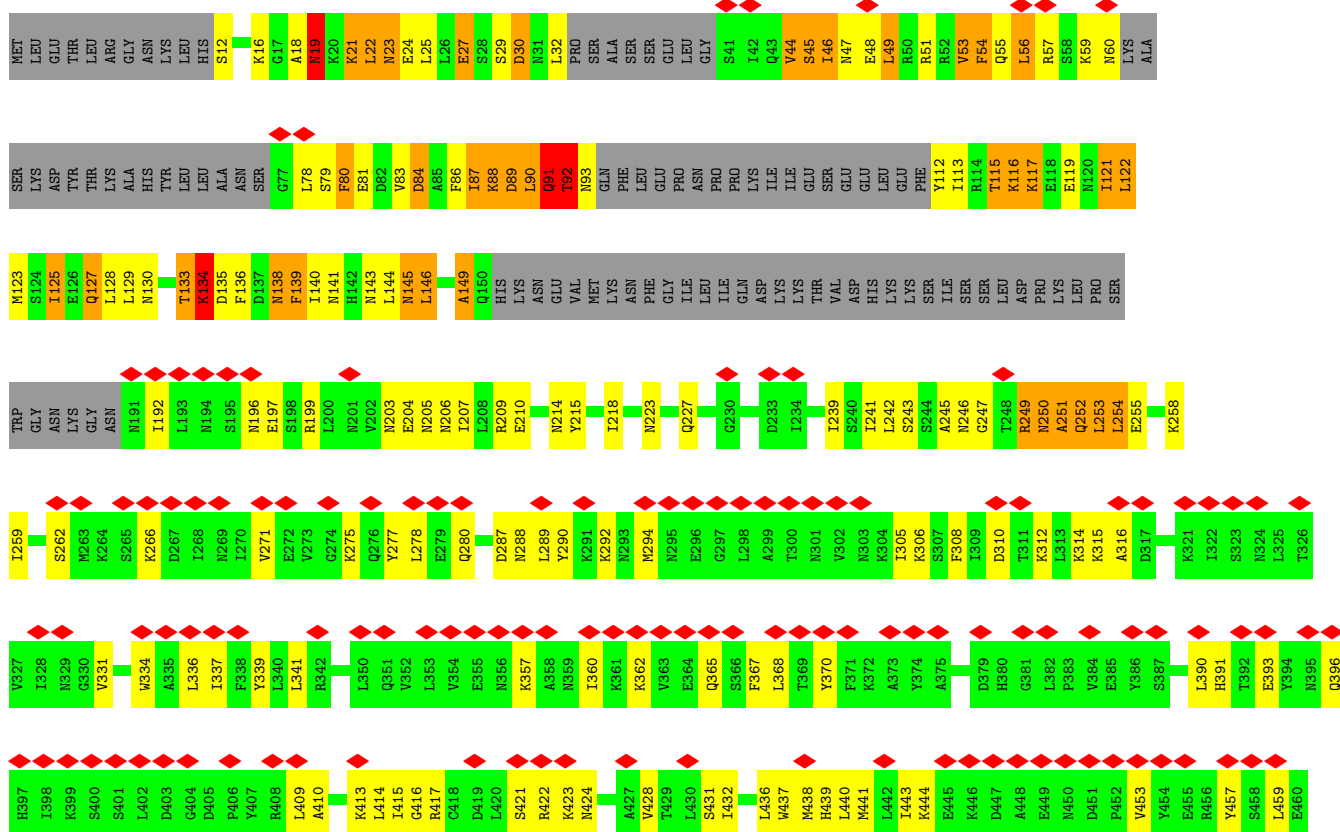


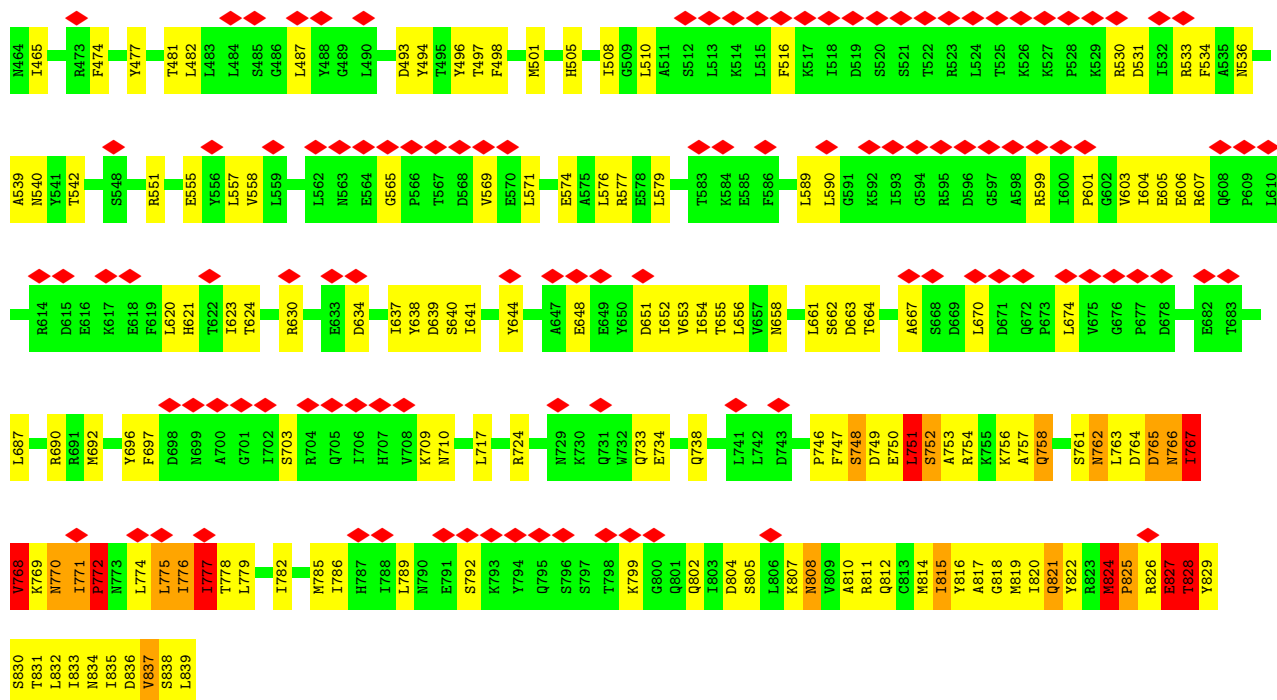
• Molecule 1: Nucleoporin NIC96





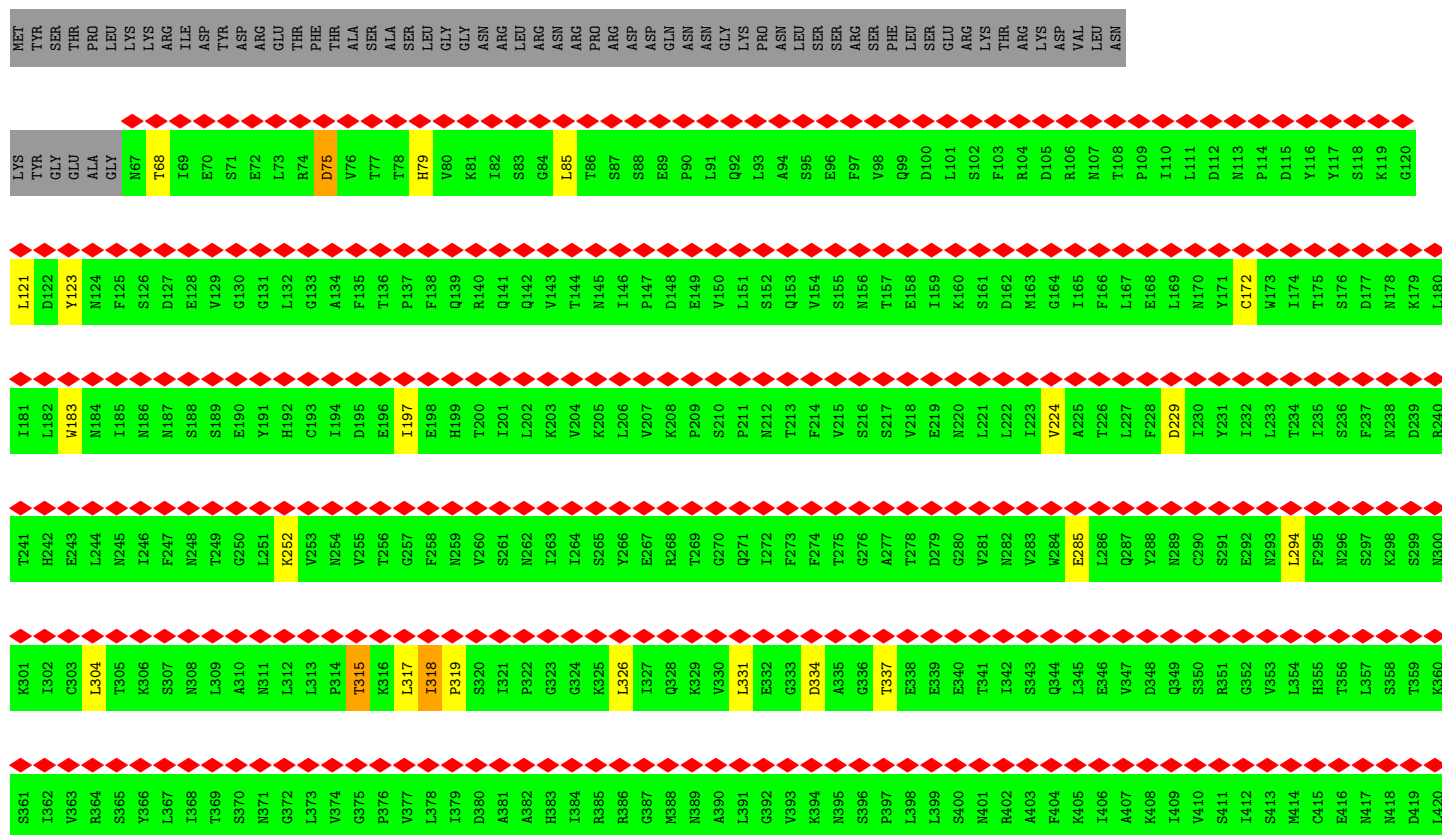
• Molecule 1: Nucleoporin NIC96



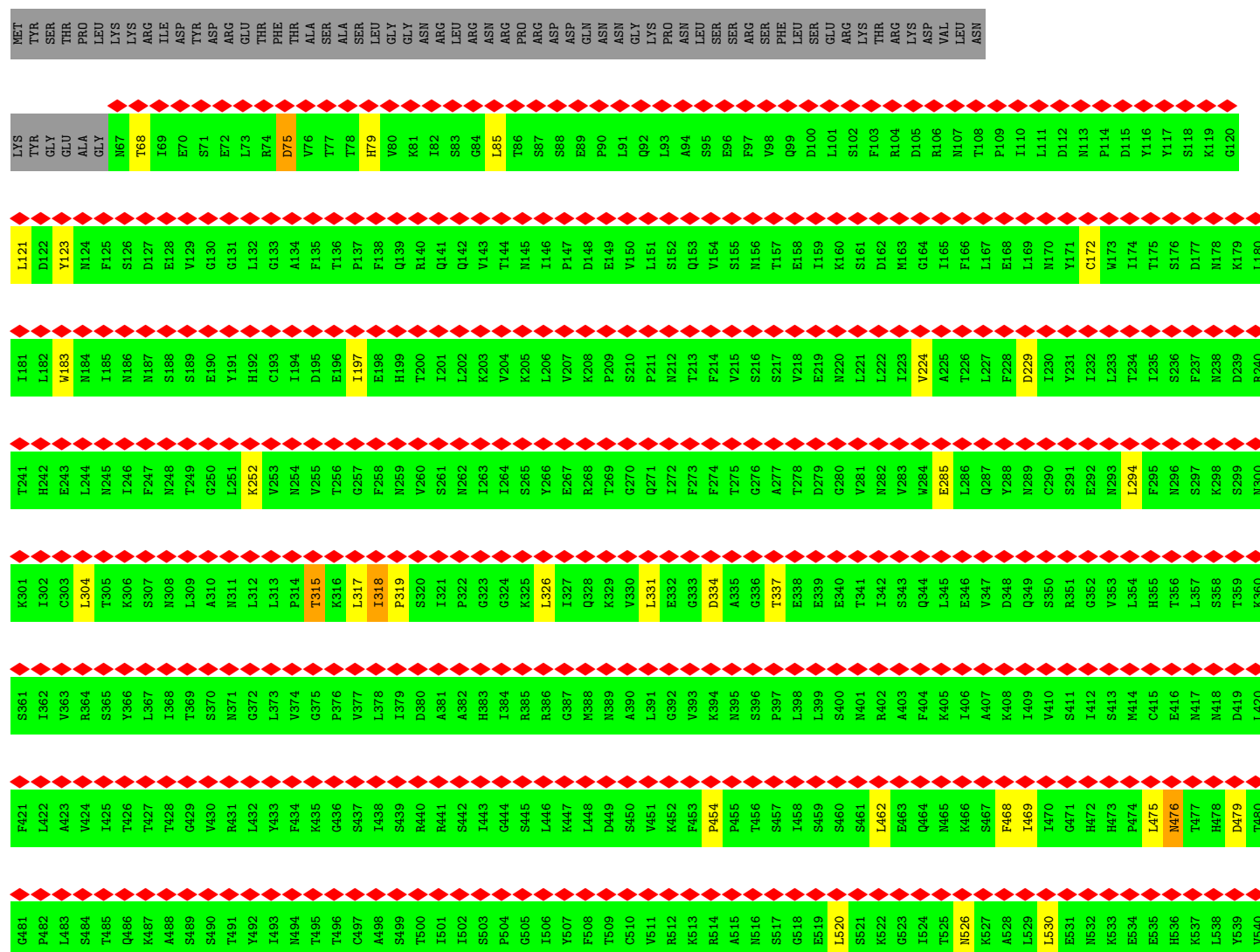


• Molecule 2: Nucleoporin NUP157

Chain C: 95%
89% 5% • 5%



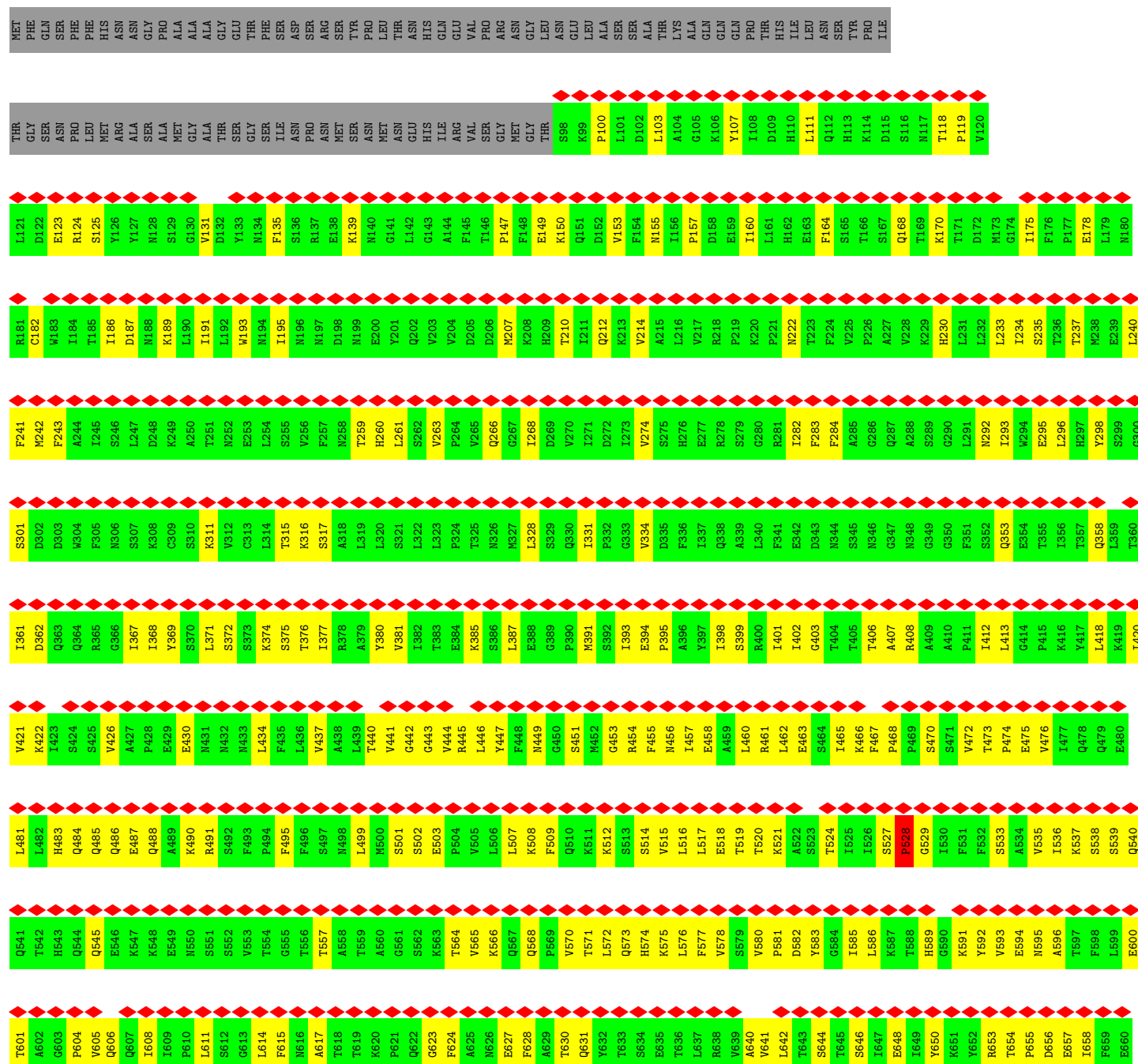
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F1147	P1082	E1022	K962	L902	E942	S782	Q722	L662	A602	A542	P482	L422
D1148	Y1083	Q1023	T963	C903	Y843	J783	I723	A663	V603	P543	L483	A423
Q1149	L1084	S1024	V964	Y904	F944	A784	W724	F664	L604	D544	S484	V424
K1150	K1085	P1025	G965	R905	F945	I785	E725	F665	T605	G545	T485	I425
P1151	E1086	S1026	F966	A906	D946	T786	E726	S666	S606	G546	Q486	T426
A1152	R1087	I1027	L967	G907	L847	A787	R727	A667	N607	I547	K487	T427
L1153	A1088	A1028	L968	E908	K948	S788	W728	G668	A608	L548	A488	T428
V1154	E1089	R969	R969	R909	F949	D789	F729	I669	L609	K549	S489	G429
Q1155	K1090	I1030	F970	L910	H850	A790	W730	P670	E610	N550	S490	V430
L1156	S1091	S1031	A971	E911	D851	E791	F731	G671	I611	Y551	T491	R431
S1157	L1092	I1032	D972	A912	L852	S792	K732	V672	Y612	G552	Y492	L432
E1158	E1093	K973	K973	A913	F953	I793	R733	G673	C613	K553	I493	Y433
M1159	I1094	S1034	I974	Q914	T854	A794	A734	E674	Y614	Y554	N494	F434
I1160	S1095	P1035	D975	K915	P855	W795	S735	I675	R615	V555	T495	K435
H1161	N1096	A1036	K976	F916	N856	W796	K736	K676	T616	E556	T496	G436
L1162	L1097	S1037	G977	E917	A857	A797	T737	P677	P617	N557	C497	S437
L1163	L1098	S1038	N978	K918	K858	L798	E738	K678	D618	T558	A498	I438
F1164	Y1099	L1039	Q979	I919	T859	I799	K739	S679	E619	A559	S499	S439
D1165	F1100	K1040	A980	D920	K860	L800	W740	S680	V620	L560	T500	R440
I1166	Y1101	K1041	Q981	S921	Q861	L801	D741	R681	F621	L561	I501	R441
L1167	L1102	R1042	E982	K922	L862	I802	A742	E682	E622	D562	I502	S442
S1168	F1103	Y1043	Y983	I923	I863	N803	F743	S683	S623	T563	S503	I443
I1169	K1104	Y1044	V984	S924	K864	S904	G744	G684	L624	T564	P504	G444
Q1170	E1105	S1045	S985	R925	E865	I805	I745	S685	I625	D565	G505	S445
D1171	E1106	V1046	R986	N926	I866	K806	S746	V686	E626	E566	I506	L446
D1172	H1107	I1047	G987	H927	L867	D807	I747	P687	N627	I567	Y507	K447
L1173	F1108	M1048	C988	L928	I868	A808	T748	P688	P628	K568	F508	L448
M1174	E1110	M1049	N989	D929	E869	L809	R749	I889	L629	E569	T509	D449
L1175	A1111	S1050	T990	T930	V670	S810	P750	S690	P630	I570	C510	S450
L1176	A1112	M1051	A991	A931	V671	L811	Q751	Q891	F631	V571	V511	V451
V1177	D1113	N1052	D992	I932	N872	I812	E752	N692	I632	P572	R512	K452
R1178	Y1114	R1053	P993	D933	A873	N813	E753	L693	H633	L573	K513	F453
M1179	L1115	F1054	R994	L934	N874	V814	Y754	F694	S634	T574	R514	P454
E1180	Y1116	F1055	K995	Y835	I875	F815	Y755	D895	Y635	R575	A515	P455
T1181	A1117	H1056	V996	E936	A876	V816	L756	K696	G636	S576	N516	T456
L1182	L1118	Y1057	F997	R937	S877	E817	S757	S697	L637	F577	S517	S457
A1119	A1119	C1058	Y998	C938	G878	D818	S758	G698	S638	N578	G518	I458
D1184	S1120	F1059	D999	A939	T879	I819	I759	E999	E839	Y579	E519	S459
E1185	D1122	Y1060	K1000	E940	S880	D820	S760	C700	A640	T580	L520	S460
D1186	S1121	D1061	R1001	N941	A881	A821	V761	D701	C641	S581	S521	S461
Y1187	D1123	W1062	I1002	I942	D882	F822	L762	G702	S642	T582	K522	L462
R1188	D1124	L1063	N1003	E943	Y883	K823	A763	I703	T643	P583	G523	E463
K1189	L1125	V1064	V1004	L944	I884	S824	D764	W704	A644	Q584	I524	Q464
Q1190	K1126	A1065	Y1005	C945	V885	L825	F765	L705	L645	G585	T525	N465
L1191	L1127	M1066	T1006	E946	N886	L826	F766	S706	Y646	Y586	N526	K466
T1192	K1067	K1067	L1007	L947	V887	N827	N767	F707	L647	A587	K527	S467
L1193	R1068	I1008	I1008	R948	L888	T828	I768	R708	A648	N588	A528	F468
K1194	Q1069	F1009	F1009	R949	K889	L829	H769	F709	C649	V589	L529	I469
L1195	D1070	E1010	E1010	V950	E990	N830	R770	Y710	K650	F590	L530	I470
M1196	Y1071	I1011	I1011	V951	R891	G831	F771	G711	F651	A591	E531	G471
G1197	L1072	V1012	V1012	D952	F892	A832	S772	S712	N652	S592	N532	H472
A1198	L1073	K1013	K1013	I953	G893	G833	F773	A713	K653	Q593	K533	H473
V1199	R1074	S1014	S1014	N954	S894	G834	W774	L714	S654	Y594	E534	P474
L1200	L1075	V1015	V1015	V955	F895	V835	S775	L715	E555	S595	E535	L475
P1201	D1076	D1016	D1016	K956	C956	Y836	F776	I716	H656	A596	H336	N476
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L1271	A1210	K1150	E1086	S1026	F966	A906	D846	T786	R726	S666	S606	G546
L1272	D1211	P1151	R1087	I1027	L967	G907	L847	A787	R727	S666	S606	L547
I1273	F1212	A1152	A1088	A1028	L968	E908	K848	S788	W728	G668	A608	L548
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T1279	L1220	I1160	N1096	A1036	X976	F916	N856	M796	K736	I675	R616	V555
D1280	R1221	H1161	L1097	S1037	G977	E917	N856	A797	T737	P677	P617	N557
V1282	I1222	E1162	L1098	S1038	N978	M918	K858	L798	E738	K678	D618	T558
F1283	F1223	L1163	W1099	L1039	Q979	I919	T859	I799	K739	S679	E619	A559
P1284	K1224	F1164	F1100	K1040	A980	D920	K860	L800	M740	S680	V620	L560
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H1286	S1226	T1166	F1103	R1042	E982	K922	L862	I802	A742	E682	E622	D562
F1287	Q1227	A1167	V1043	V1044	Y984	I923	I863	N803	F743	S683	E622	D562
L1288	F1228	S1168	E1105	Y1044	N984	S924	K864	S804	G744	G684	L624	T564
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N1290	D1230	Q1170	E1106	V1046	N986	N926	I866	K806	S746	V686	E626	E566
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L1293	V1233	L1173	L1109	N1049	N989	D929	E869	L809	R749	I689	L629	E569
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S1295	Q1235	M1175	A1111	M1051	A991	A931	V871	L811	Q751	Q691	F631	V571
F1296	G1236	L1176	A1112	N1052	D992	I932	N872	I812	V752	N692	I632	P572
I1297	E1237	V1177	D1113	R1053	P993	D933	A873	N813	E753	L693	H633	L573
D1298	W1238	R1178	L1115	F1054	R994	L934	N874	V814	Y754	F694	S634	T574
K1299	N1239	M1179	V1116	F1055	X995	Y935	I875	F815	Y755	D695	Y635	R575
S1300	R1240	E1180	A1117	H1056	V996	E936	A876	Y816	L756	K696	G636	S576
S1301	L1241	T1181	A1117	Y1057	F997	R937	S877	E817	S757	S697	G636	F577
A1302	L1242	R1182	L1118	C1058	Y998	C938	G878	D818	S758	G698	S638	N578
A1303	D1243	I1183	A1119	F1059	D999	C939	T879	D819	I759	E699	E639	Y579
D1304	S1244	D1184	S1120	Y1060	K1000	E940	S880	D820	S760	C700	A640	T580
G1305	M1245	E1185	S1121	D1061	R1001	N941	A881	A821	V761	D701	C641	S581
S1306	K1246	D1186	D1122	W1062	I1002	I942	D882	F922	L762	G702	S642	T582
C1307	N1247	Y1187	F1123	L1063	N1003	E943	R883	K823	A763	I703	T643	P583
L1308	A1248	K1188	D1124	V1064	V1004	L944	I884	S824	D764	V704	A644	Q584
S1309	P1249	K1189	L1125	A1065	Y1005	C945	V885	L825	F765	L705	L645	G585
M1310	S1250	Q1190	K1126	N1066	T1006	E946	N886	L826	F766	S706	Y646	Y586
L1312	D1252	L1191	L1127	K1067	L1007	E947	V887	N827	T67	P707	L647	N587
L1313	V1253	T1192	S1128	K1068	I1008	R948	L888	T828	I768	R708	A648	A588
A1314	G1254	K1194	E1129	Q1069	F1009	R949	K889	L829	H769	F709	C649	V589
G1315	S1255	L1195	R1130	D1070	E1010	V950	E990	M830	R770	Y710	K650	F590
V1316	V1256	M1196	T1131	Y1071	I1011	R951	R891	G831	P771	G711	F651	A591
S1317	W1257	G1197	E1132	L1072	V1012	D952	F892	A832	S772	S712	N652	S592
H1318	Q1258	R1198	W1138	L1073	K1013	I953	G893	G833	F773	A713	K653	Q593
L1319	E1259	V1199	G1139	R1074	S1014	M954	S894	G834	V774	L714	S654	Y594
K1320	S1260	L1200	L1140	L1075	V1015	V955	F895	R835	S775	L715	E655	S595
L1321	F1261	P1201	C1141	D1076	D1016	K956	C996	Y836	F776	I716	H656	A596
Y1322	L1262	L1202	D1142	S1077	D1017	L957	H897	D837	V777	T717	I657	E597
S1323	S1263	L1203	S1143	Q1078	Y1018	N958	S898	S838	P778	R718	K658	P598
L1324	S1264	D1204	S1144	V1080	T1019	Y959	A899	T840	F779	L719	S660	K600



● Molecule 3: Nucleoporin NUP170



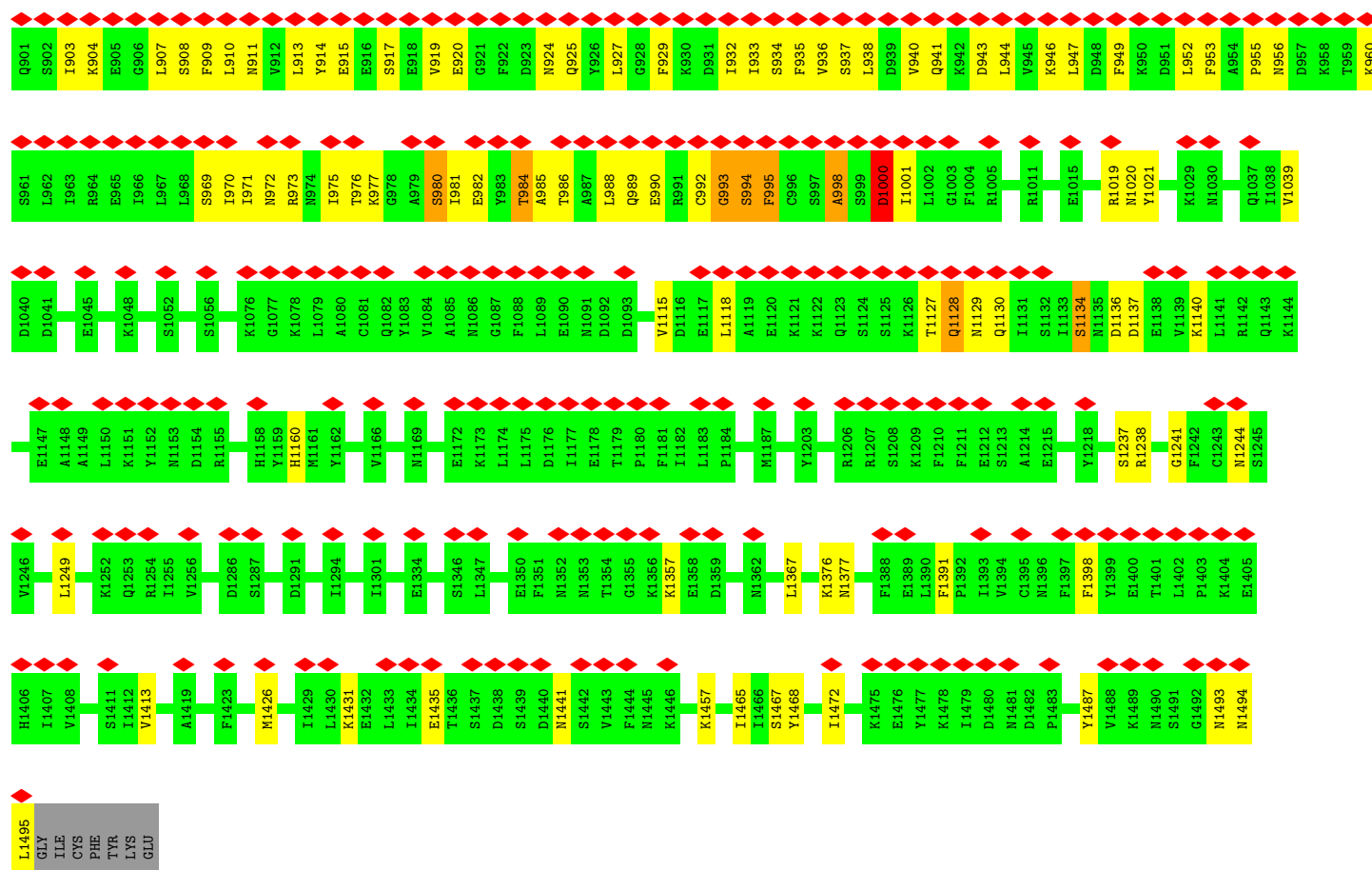
D661	L781	Y841	Q901	S961	V1039	R1142	C1243	P1403	G1492
L662	V721	Y842	S902	L962	D1040	Q1143	N1244	K1404	N1493
I663	S723	L843	I903	I963	D1041	K1144	S1245	E1405	N1494
D664	T724	S844	K904	R964	E1045	E1147	L1249	H1406	L1495
N665	S725	S845	G906	E965	K1048	A1148	K1252	T1407	GLY
P666	S726	I846	L907	I966	S1052	A1149	Q1253	V1408	CYS
L667	S727	N847	S908	L967	K1056	L1150	I1254	S1411	PHE
P668	L728	I948	F909	L968	S1056	K1151	I1255	I1412	TYR
P669	L729	L849	S910	S969	N1072	Y1152	V1256	Y1413	LYS
V670	S730	N850	N911	I970	K1076	N1153	D1286	A1419	GLU
L671	K731	E951	V912	I971	G1077	D1154	S1287	F1423	
N672	P732	F952	L913	R973	K1078	R1155	I1291	M1426	
Y673	T733	I954	Y914	N974	G1079	H1158	I1294	T1429	
G674	L734	I955	E915	T975	A1080	Y1159	I1301	E1432	
A675	S735	T956	E916	T976	C1081	M1160	E1334	L1433	
A676	T736	Y956	G917	K977	Y1082	Y1162	S1346	I1434	
E677	A737	G957	S918	G978	N1085	I1166	L1347	E1435	
A678	T738	D958	E919	A979	N1086	V1166	E1350	T1436	
C679	T739	S959	V919	S980	F1088	N1169	F1351	D1438	
S680	N740	I860	E920	I981	G1089	E1172	N1352	S1439	
T681	L741	S961	G921	E982	E1090	L1174	I1353	D1440	
A682	Q742	Q962	F922	Y983	F1089	L1175	N1357	N1441	
L683	Q743	I863	D923	T984	E1091	L1176	E1358	S1442	
F684	S744	S964	N924	T986	N1091	D1177	D1359	V1443	
F685	I745	A965	Q925	A987	E1092	E1178	M1362	N1444	
T686	T746	P966	Y926	L988	D1093	I1179	L1367	N1445	
C687	G747	Y967	L927	Q989	V1115	P1180	K1376	K1446	
K688	F748	V968	G928	E990	D1116	F1181	N1377	K1457	
S689	S749	L869	F929	E991	E1117	I1182	F1388	I1465	
N690	K750	P809	K930	C992	L1118	L1183	E1389	I1466	
K691	P751	T811	D931	G993	A1119	P1184	L1390	S1467	
S692	S752	P812	I932	S994	E1120	M1187	F1391	Y1468	
E693	P753	S813	I933	P995	K1121	Y1203	P1392	I1472	
K694	A754	I814	S934	C996	Q1122	R1206	I1393	K1475	
L695	N755	N815	F935	S997	S1125	R1207	V1394	E1476	
R696	K756	N816	V936	A998	T1127	S1208	C1395	Y1477	
S697	E757	L817	S937	S999	Q1128	K1209	N1396	K1478	
N698	D758	K818	L938	D1000	Q128	F1210	F1397	I1479	
A699	F759	S819	D939	I1001	E1129	F1211	F1398	D1480	
L700	D760	D820	V940	L1002	Q1130	E1212	I1399	N1481	
T701	L761	E821	Q941	G1003	I1131	S1213	V1399	D1482	
F702	D762	I822	K942	F1004	I1132	A1214	C1396	P1483	
L703	D763	S823	D943	R1005	Q1133	E1215	F1397	Y1487	
T704	V764	Q824	L944	R1011	I1134	E1216	F1398	V1488	
N705	I765	N825	V945	E1015	S1134	Y1218	I1399	K1489	
G706	L766	R826	K946	L1018	D1135	S1237	E1400	N1490	
I707	S767	N827	L947	R1019	N1136	R1238	T1401	S1491	
P708	P768	I828	D948	Y1021	D1137	G1241	L1402		
G709	F769	I829	F949	K1029	E1138	F1242	L1402		
V710	T770	S830	K950	N1030	V1139				
V711	Y771	K831	D951	K1037	E1139				
D712	G772	V832	L952	I1038	V1140				
I713	T773	S833	F953		L1141				
K714	A774	I834	A954						
P715	L775	S835	P955						
V716	L776	K836	N956						
Y717	I777	D837	D957						
N718	T778	C838	K958						
R719	R779	T839	T959						
Y720	L780	V900	K960						

• Molecule 3: Nucleoporin NUP170

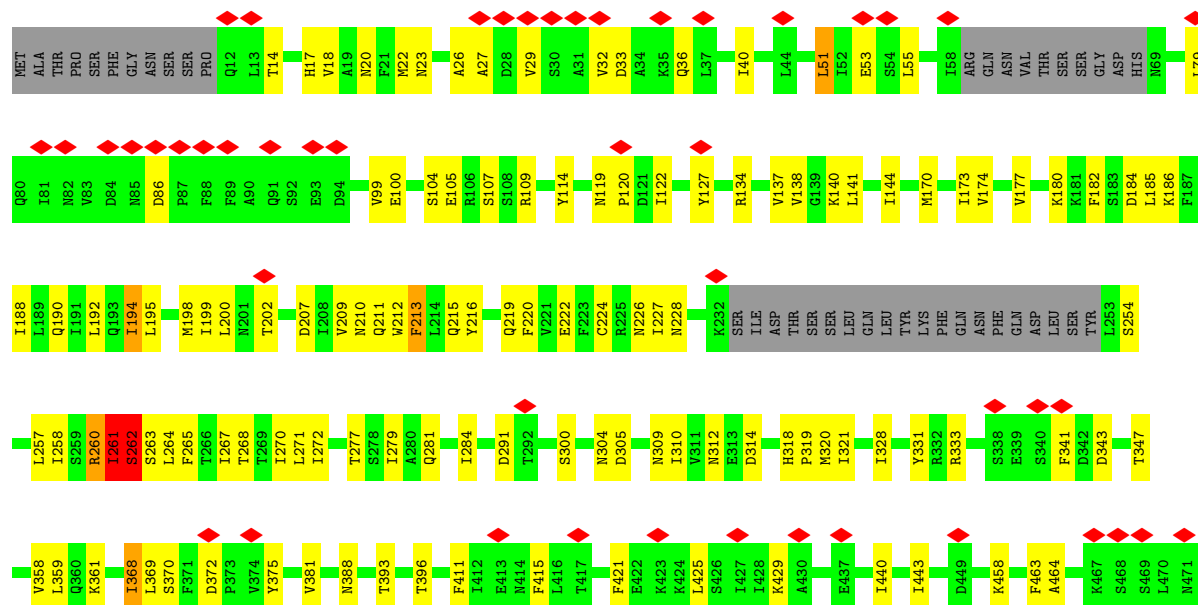
Chain P: 66% 26% 7%

MET	PHE	GLN	SER	PHE	PHE	HIS	ASN	ASN	GLY	THR	PHE	PHE	SER	ASP	SER	SER	ARG	SER	TYR	PRO	LEU	THR	ASN	HIS	GLN	GLU	VAL	PRO	ARG	ASN	GLY	LEU	ASN	GLU	LEU	ALA	SER	SER	ALA	THR	LYS	ALA	GLN	GLN	PRO	THR	HIS	ILE	LEU	ASN	SER	TYR	PRO	ILE
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THR	GLY	SER	ASN	PRO	LEU	MET	ARG	ALA	SER	ALA	GLY	ALA	THR	SER	GLY	SER	ILE	ASN	PRO	ASN	MET	SER	ASN	GLY	THR	S98	K99	P100	L101	D102	L103	A104	G105	K106	Y107	I108	D109	H110	L111	Q112	H113	K114	D115	S116	N117	T118	P119	V120																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						

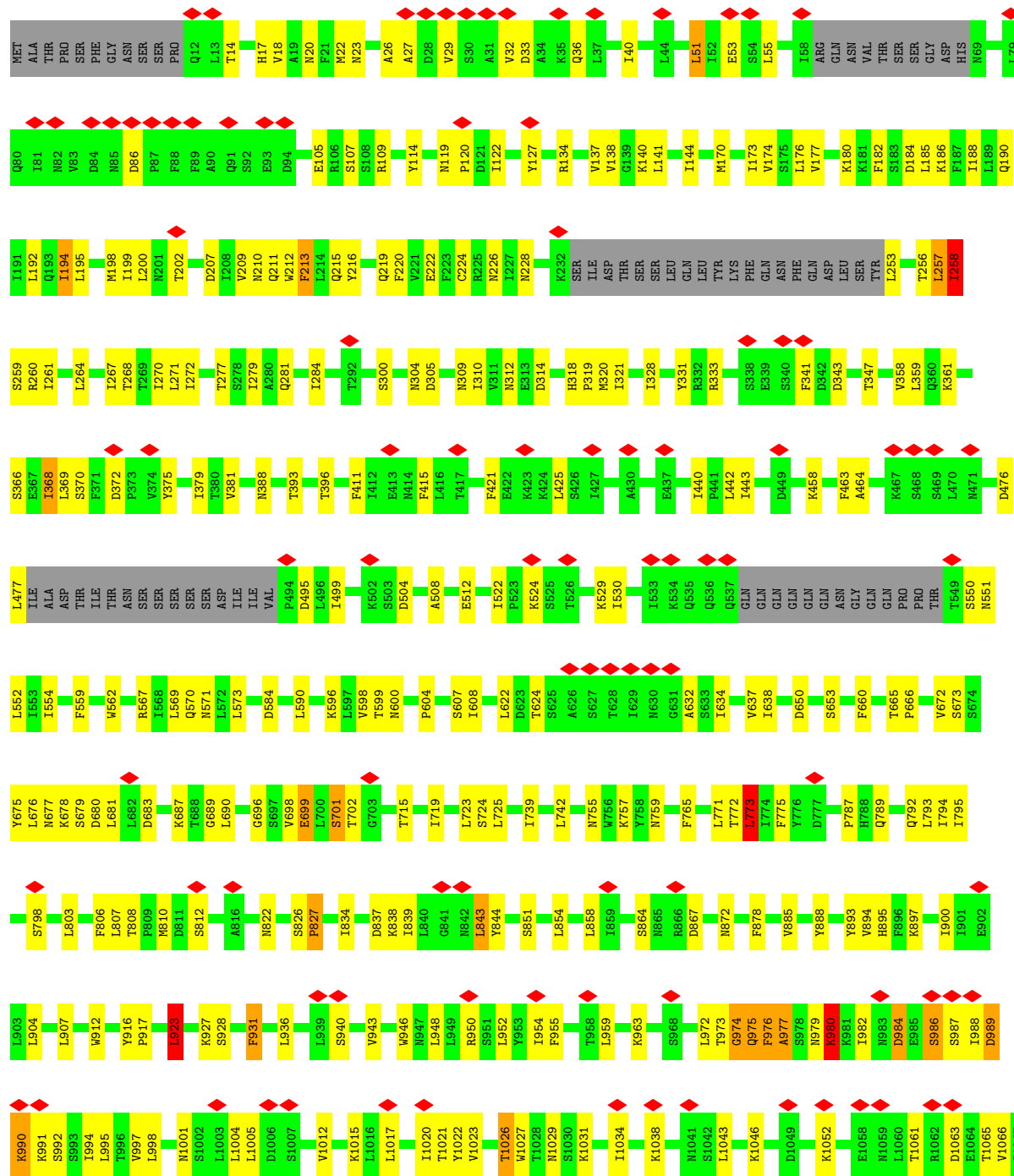


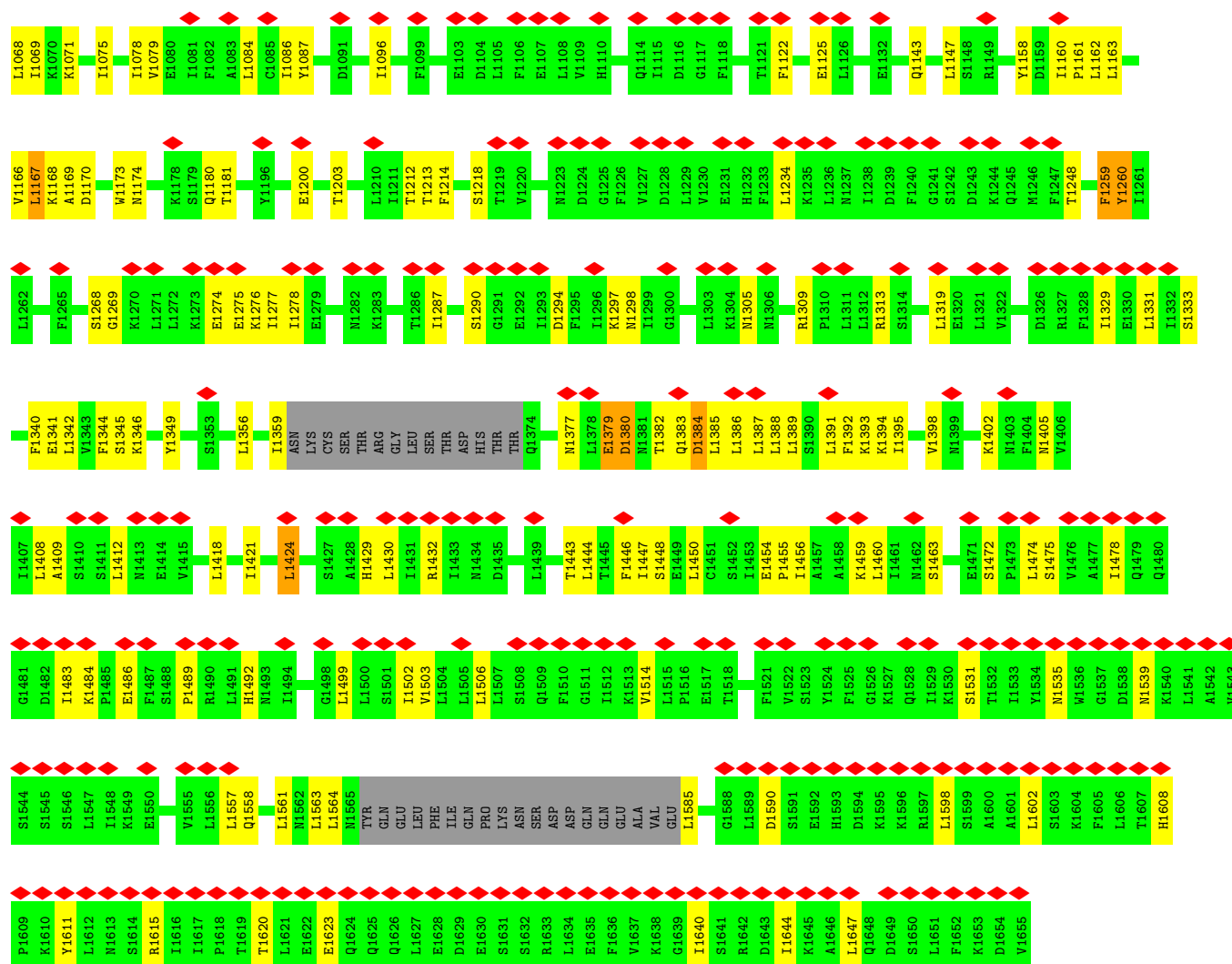
• Molecule 4: Nucleoporin NUP188





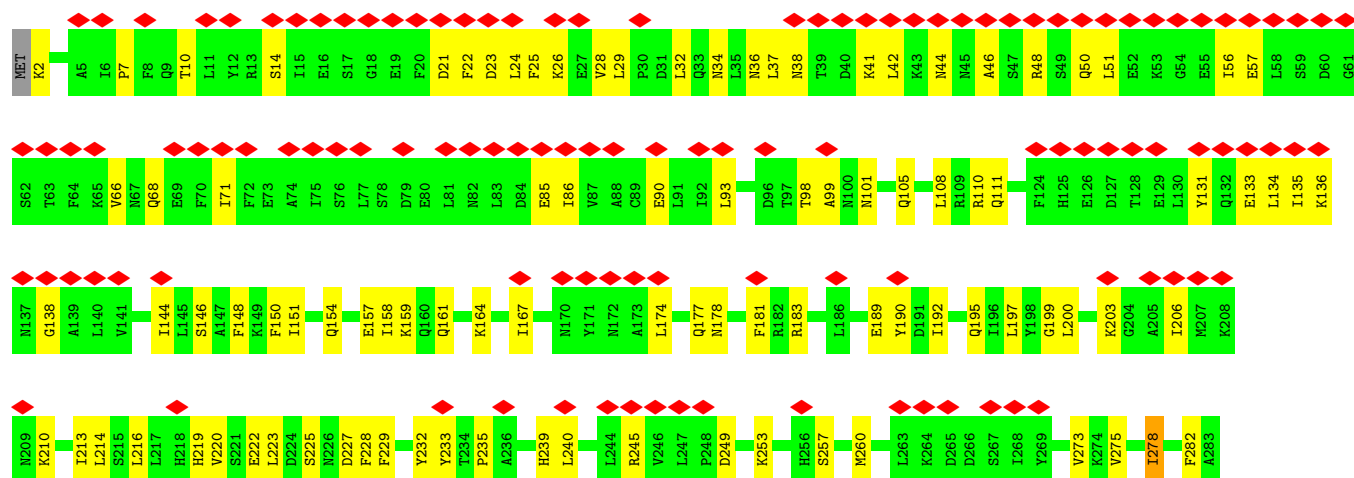
● Molecule 4: Nucleoporin NUP188



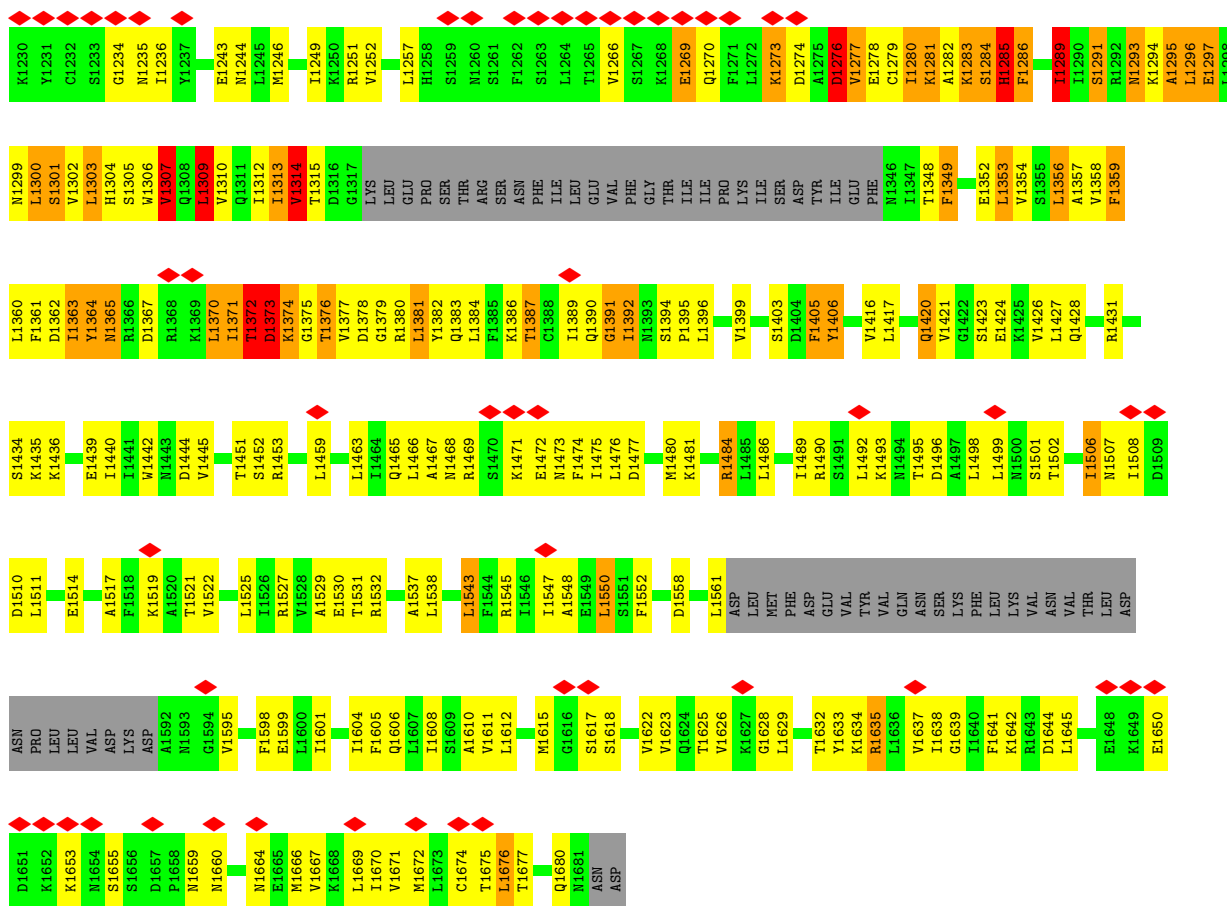


• Molecule 5: Nucleoporin NUP192

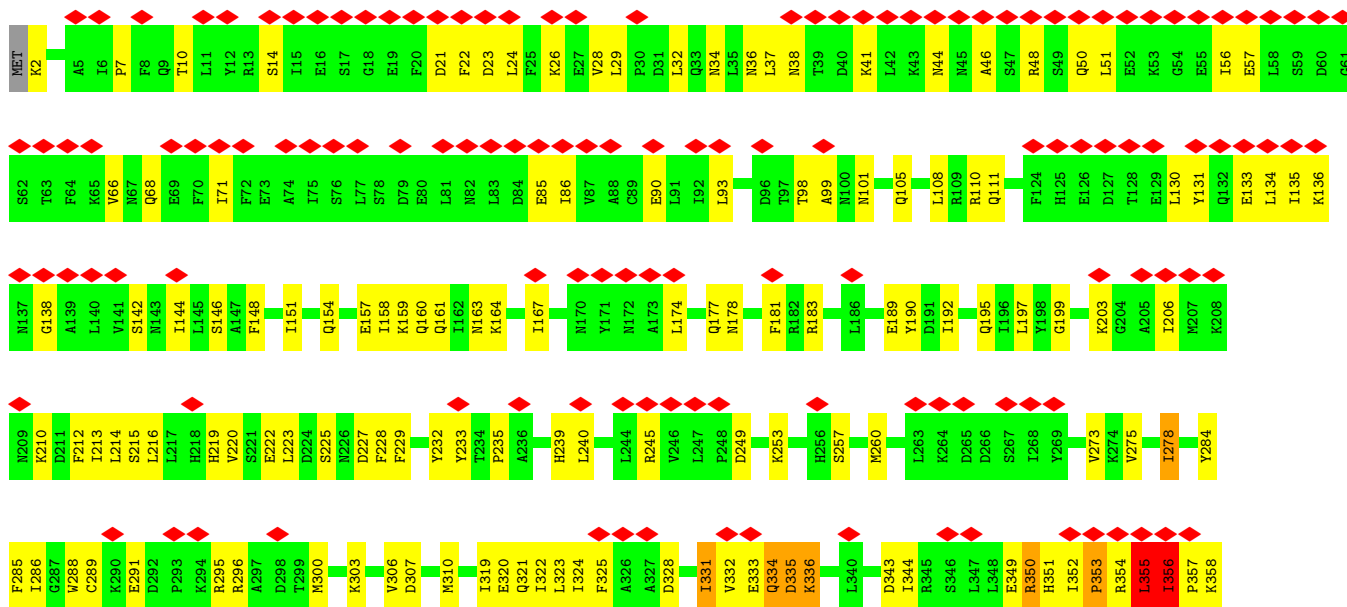
Chain F: 23% 49% 37% 7%

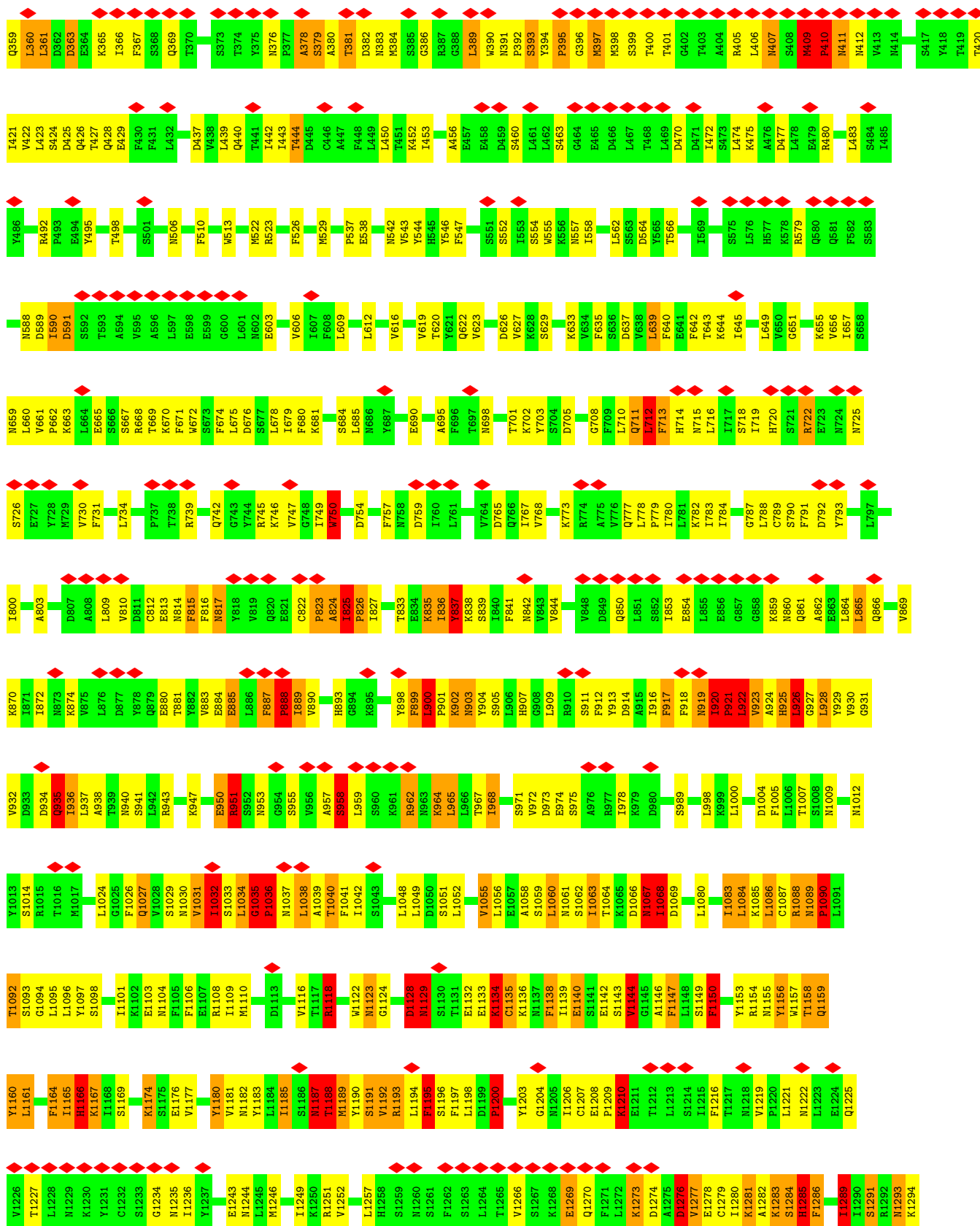


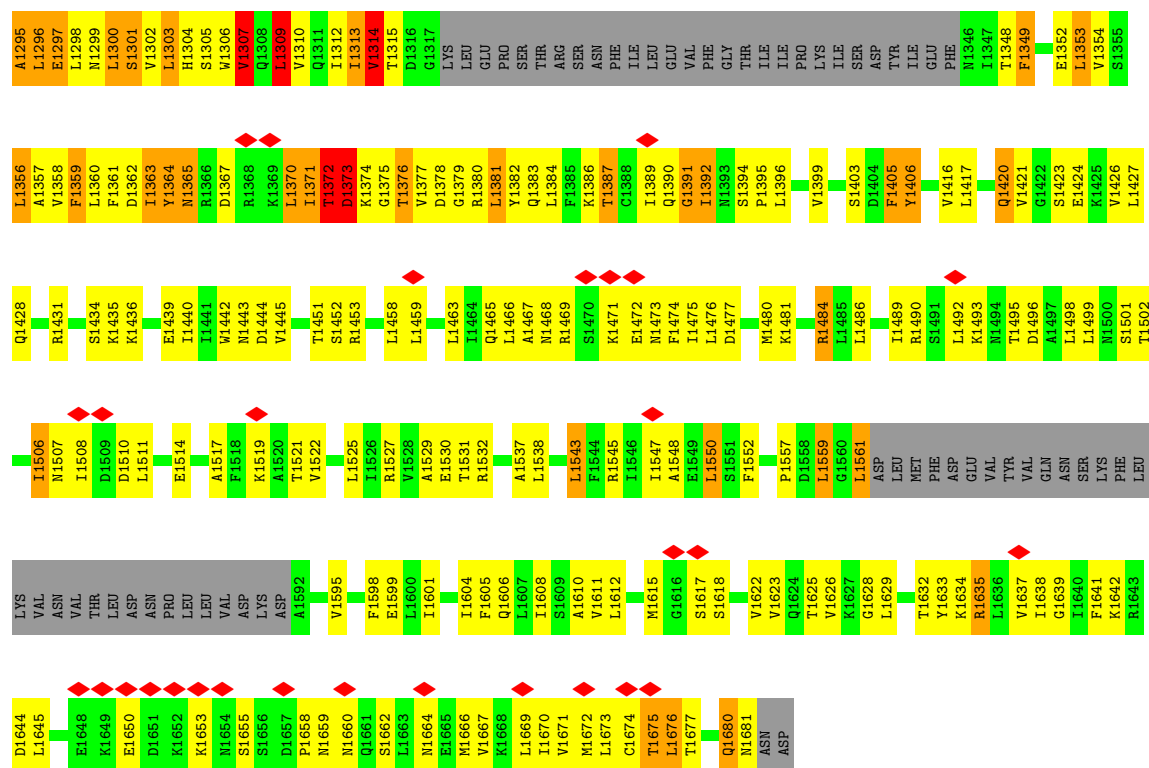




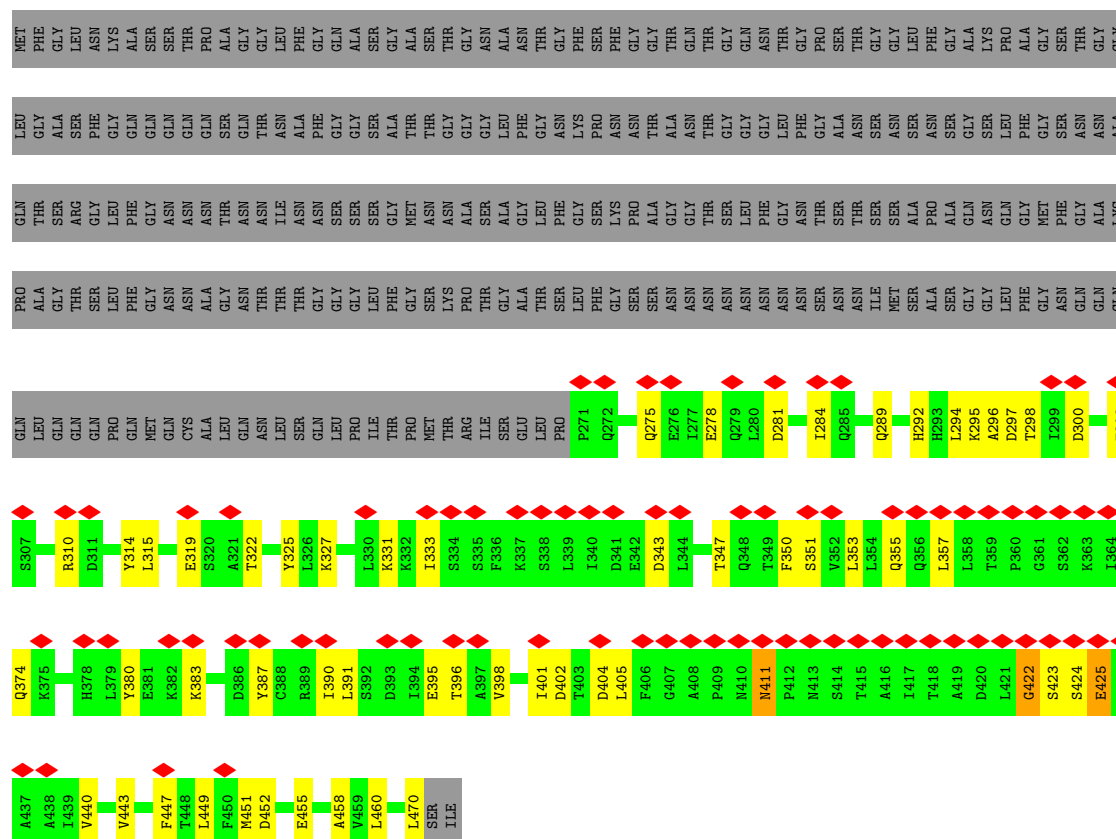
• Molecule 5: Nucleoporin NUP192







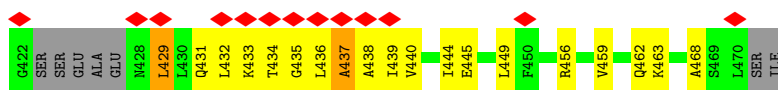
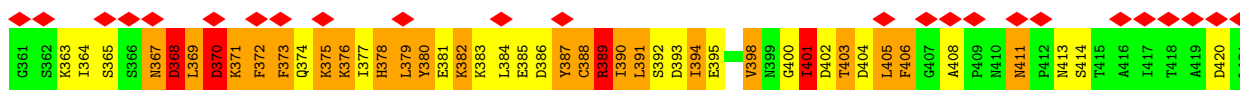
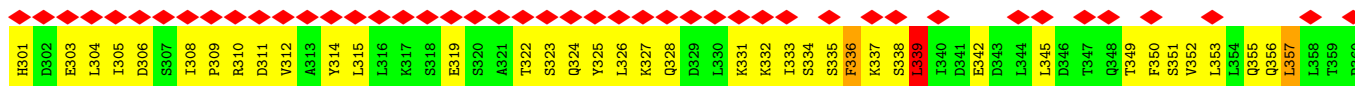
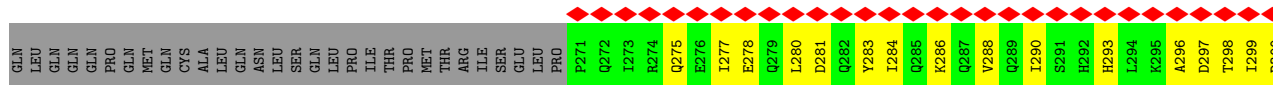
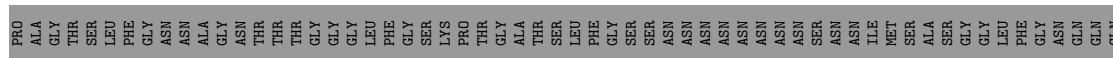
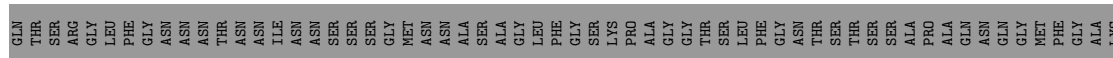
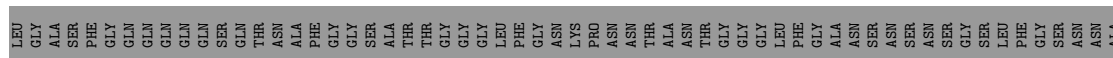
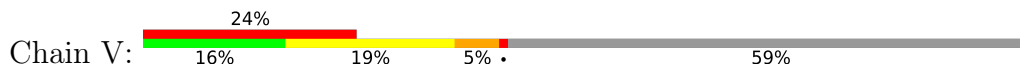
• Molecule 6: Nucleoporin NUP49/NSP49



Chain J:

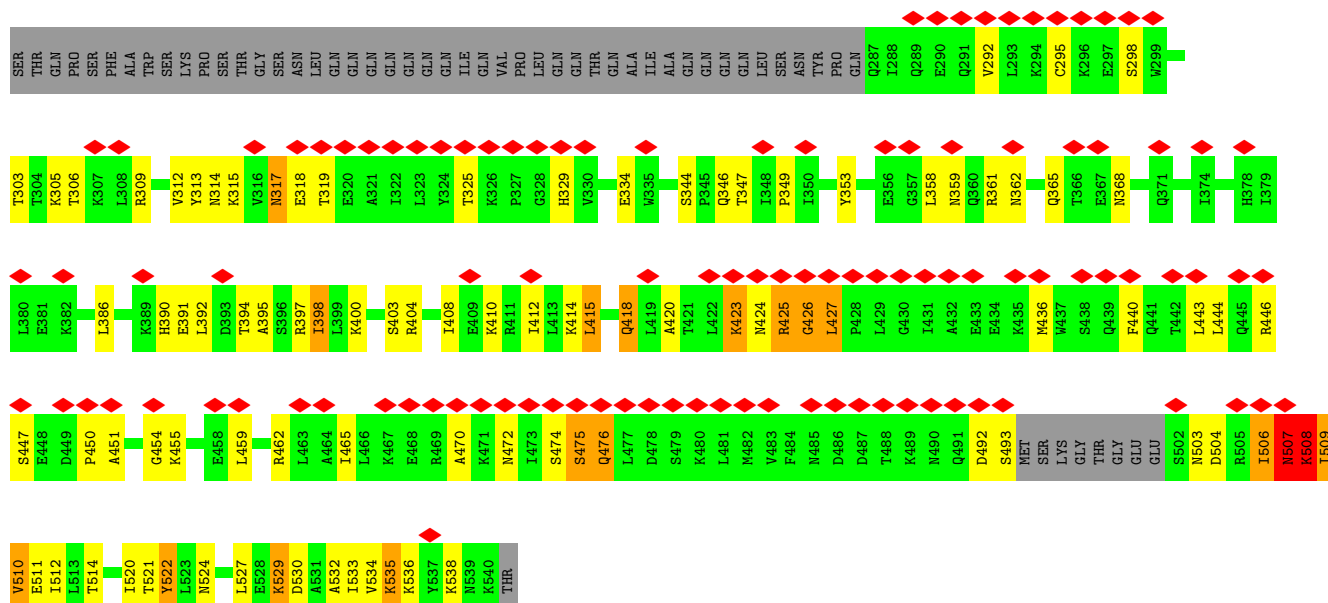


- Molecule 6: Nucleoporin NUP49/NSP49

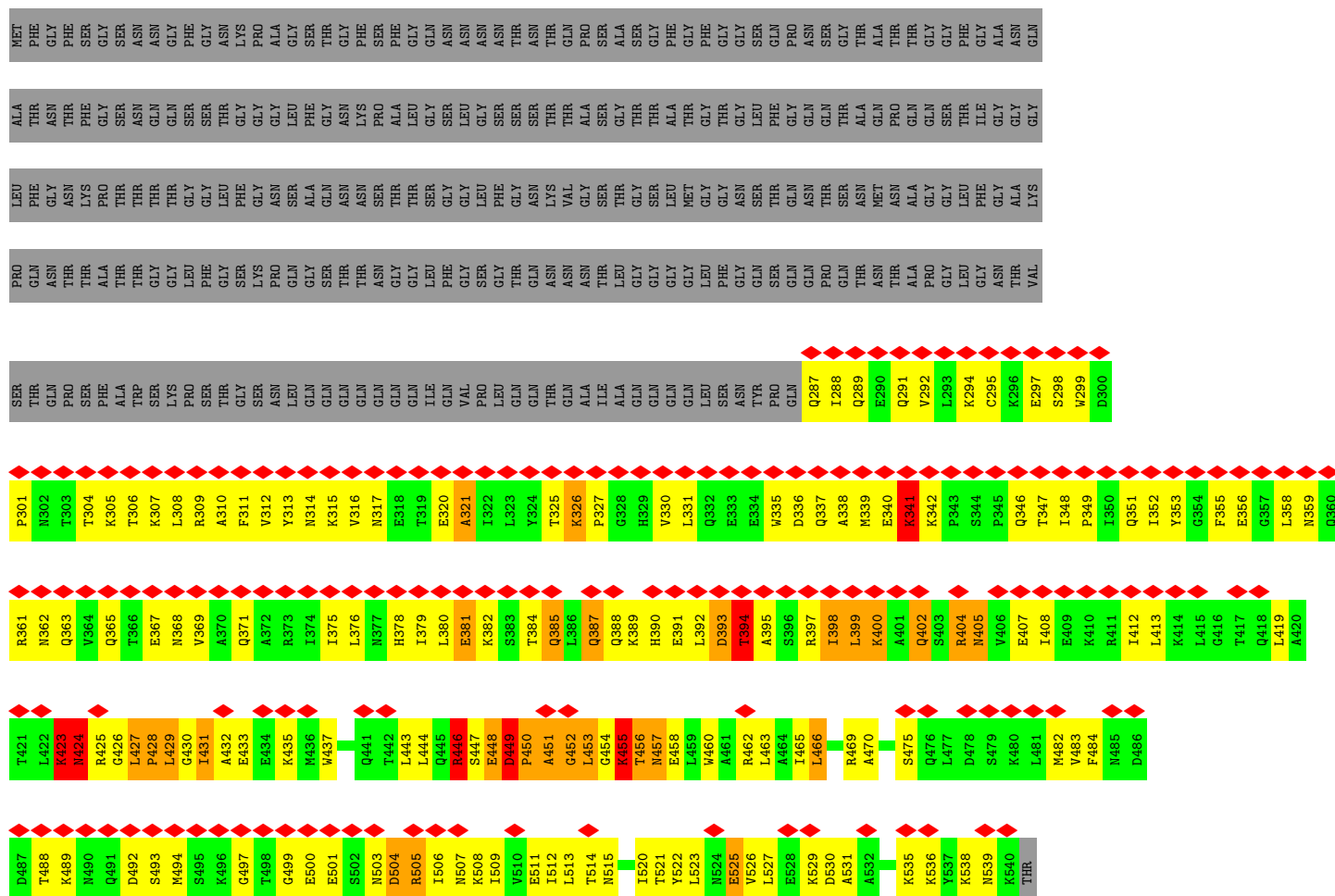
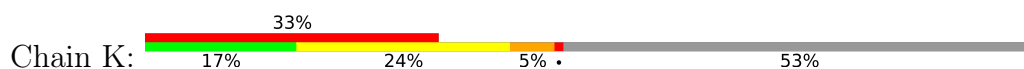


- Molecule 7: Nucleoporin NUP57





• Molecule 7: Nucleoporin NUP57



Chain T:



NET	PHE	GLY	PHE	SER	SER	ASN	GLY	PHE	GLY	GLY	ASN	LYS	PRO	ALA	GLY	SER	THR	GLY	GLN	ASN	ASN	ASN	ASN	THR	THR	GLN	PRO	PRO	GLN	SER	ALA	SER	GLY	GLY	PHE	GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR	THR	THR	ALA	ALA	ALA	ALA	ASN	ASN
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ALA	THR	THR	THR	PHE	GLY	SER	ASN	GLN	GLN	SER	SER	THR	GLY	GLY	LEU	PHE	GLY	ASN	LYS	PRO	PRO	ALA	ALA	LEU	GLY	SER	SER	SER	THR	THR	THR	THR	THR	GLY	LEU	PHE	GLY	GLN	GLN	THR	ALA	GLN	GLN	PRO	PRO	GLN	GLN	SER	SER	THR	THR	ILE	GLY	GLY	GLY
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PRO	GLN	ASN	THR	THR	ALA	THR	THR	GLY	GLY	LEU	PHE	GLY	LYS	SER	PRO	GLN	GLN	GLY	SER	THR	THR	ASN	ASN	GLN	ASN	ASN	THR	THR	LEU	GLY	GLY	GLY	GLY	PHE	GLN	GLN	SER	GLN	GLN	GLN	PRO	GLN	THR	THR	THR	ALA	PRO	GLY	LEU	GLY	GLY	ASN	THR
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SER	THR	GLN	PRO	SER	PHE	ALA	TRP	SER	LYS	PRO	SER	THR	GLY	SER	ASN	LEU	GLN	GLN	GLN	GLN	GLN	ILE	GLN	GLN	VAL	PRO	PRO	LEU	GLN	GLN	THR	GLN	ALA	ALA	ILE	ALA	GLN	GLN	GLN	GLN	GLN	LEU	SER	ASN	TYR	PRO	GLN	PRO	Q287	Q288	Q289	Q290	Q291	Q292	Q293	Q294	Q295	Q296	Q297	Q298	Q299
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T803	T904	K305	T906	K307	L308	R309	V310	V312	V313	N314	K315	V316	N317	E318	T319	E320	A321	I322	L323	Y324	T325	K326	P327	G328	H329	V330	E334	W336	S344	P345	Q346	T347	F348	L349	I350	Y353	E356	G357	L358	N359	K360	N362	Q365	T366	F367	N368	O371	I374	H376	T378
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L380
E381
S382
S383
T384
Q385
L386

K389
H390
E391
L392
D393
T394
S396
R397
I398
K399
L400
S403
R404
I408
F409
K410
R411
I412
L413
K414
L415
Q418
L419
A420
T421
L422
K423
N424
R425
G426
L427
P428
L429
G430
I431
A432
E433
E434
K435
M436
W437
S438
Q439
F440
Q441
T442
L443

Q445	R446	S447	E448	D449	P450	A451	G454	K455	E458	L459	R462	L463	A464	I465	L466	K467	E468	R469	A470	K471	A472	I473	S474	S475	Q476	L477	D478	S479	K480	L481	M482	V483	F484	N485	D486	D487	T488	K489	N490	Q491	D492	A493	MET	SER	LYS	GLY	THR	GLY	GLU	GLU	S502	N503	D504	R505	I506	E507
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K508	I509	V510	E511	I512	L513	T514	I520	T521	Y522	L523	N524	L527	E528	K529	D530	A531	A532	I533	V534	K535	K536	Y537	K538	N539	K540	THR
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Chain W:

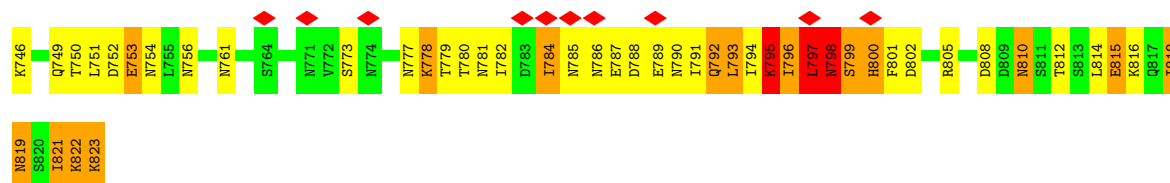


MET	PHE	GLY	GLY	PHE	SER	GLY	SER	ASN	ASN	GLY	GLY	PHE	GLY	GLY	GLY	GLN	THR	THR	THR	THR	THR	GLY	PHE	GLY	ALA	GLY	ALA	ASN
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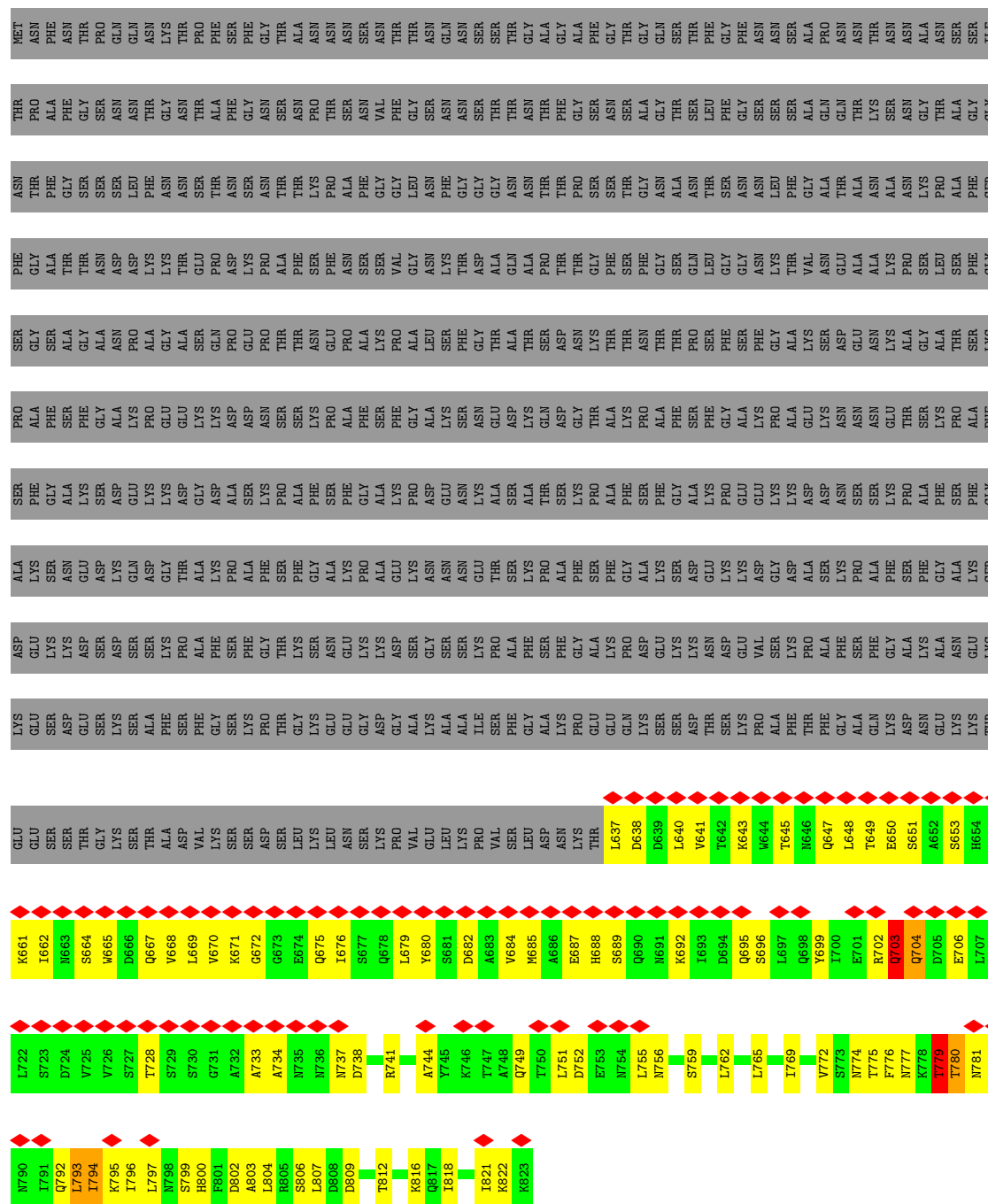
ALA	THR	ASN	PHE	GLY	SER	ASN	GLN	SER	SER	THR	GLY	GLY	LEU	PHE	GLY	ASN	LYS	PRO	ALA	ALA	LEU	GLY	SER	SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	GLY	LEU	PHE	GLY	GLN	GLN	GLN	THR	THR	ALA	ALA	GLN	GLN	PRO	GLN	GLN	SER	THR	THR	ILE	GLY	GLY
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PRO	GLN	ASN	THR	THR	ALA	THR	THR	THR	GLY	GLY	LEU	PHE	GLY	SER	LYS	PRO	PRO	GLN	GLY	SER	THR	THR	ASN	ASN	GLY	GLY	LEU	PHE	GLY	GLY	GLY	GLY	GLY	THR	GLN	ASN	ASN	THR	THR	LEU	GLY	GLY	GLY	GLY	PHE	GLN	GLN	SER	SER	GLN	GLN	PRO	GLN	THR	THR	ALA	GLY	LEU	GLY	ASN	THR.
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[illegible]



• Molecule 8: Nucleoporin NSP1



• Molecule 8: Nucleoporin NSP1

E789	L722	K661	GLU	LYS	ASP	ALA	SER	SER	GLY	ASN
N790	S723	I662	GLU	SER	GLU	LYS	SER	PHE	THR	ASN
I791	D724	N663	GLU	ASP	GLU	LYS	ASN	SER	GLY	PHE
L792	S725	S664	THR	THR	ASP	ASP	GLU	LYS	THR	GLY
L793	S726	S665	GLY	SER	SER	SER	ASP	SER	ALA	THR
I794	S727	D666	LYS	LYS	ASP	ASP	LYS	ASP	ALA	ASN
K795	T728	Q667	SER	SER	SER	SER	GLN	ASP	ASP	LEU
I796	T729	V668	THR	ALA	SER	LYS	GLY	LYS	LYS	PHE
L797	S730	L669	ALA	PHE	PRO	PRO	THR	ASP	GLU	ASN
S799	S731	V670	ASP	PHE	ALA	ALA	ALA	GLY	THR	ASN
H800	G731	V671	VAL	GLY	PHE	LYS	LYS	GLY	THR	ASN
F801	A732	K671	SER	LYS	PHE	PHE	ALA	ASP	GLU	THR
D802	A733	G672	SER	THR	THR	GLY	SER	PRO	THR	THR
A803	S734	G673	SER	GLY	LYS	LYS	PHE	SER	ALA	THR
L804	N735	S674	LEU	LYS	SER	SER	GLY	SER	LYS	THR
R805	N736	Q675	LYS	LYS	GLY	GLY	ALA	LYS	PHE	LYS
S806	N737	I676	LEU	GLU	GLY	GLY	ALA	PRO	ASN	PHE
L807	N738	S677	ASN	GLY	LYS	PRO	GLY	ALA	SER	GLY
D808	D738	S677	SER	GLY	LYS	ALA	ALA	SER	LYS	GLY
D809		Q678	LYS	ASP	LYS	ALA	LYS	PRO	PRO	GLY
	R741	L679	PRO	GLY	ASP	GLU	LYS	PHE	VAL	LEU
T812		L679	VAL	ALA	GLY	LYS	LYS	GLY	ALA	ASN
K816	A744	V680	GLU	LYS	GLY	ASN	ASN	ALA	LEU	ASN
G817	Y745	S681	LEU	ALA	SER	ASN	GLY	LYS	SER	PHE
I818	K746	D682	LYS	LYS	SER	ASN	LYS	SER	PHE	GLY
	T747	A683	PRO	ILE	LYS	GLY	LYS	ASN	GLY	GLY
I821	A748	V684	VAL	SER	PRO	THR	THR	GLU	ALA	GLY
K822	Q749	S685	SER	GLY	PHE	LYS	LYS	ASP	ALA	ASN
K823	T750	A686	ASN	LYS	PHE	ALA	GLY	GLY	THR	ASN
	L751	E687	ASN	LYS	GLY	LYS	LYS	ASN	THR	ASN
	D752	H688	LYS	GLU	ALA	LYS	PHE	GLY	THR	THR
E753	E753	S689	THR	GLU	ALA	ALA	PHE	THR	GLY	SER
L755	N754	Q690		GLN	PRO	LYS	ALA	ALA	THR	THR
N756	N756	N691	D638	LYS	GLU	GLY	GLY	LYS	THR	THR
		K692	D639	SER	LYS	LYS	LYS	ALA	THR	PRO
	S759	I693	L640	SER	GLU	LYS	SER	PHE	THR	SER
		D694	V641	ASP	LYS	LYS	ASP	SER	PRO	ALA
L762	L762	D694	T642	THR	ASN	ASN	GLY	PHE	GLY	ASN
L765	L765	Q695	K643	LYS	GLU	LYS	LYS	GLY	GLY	THR
I766	I766	S696	K644	PRO	VAL	ASP	GLU	LYS	ALA	LEU
		L697	T645	ALA	SER	GLY	GLY	LYS	PRO	PHE
	I769	Q698	K646	PHE	LYS	ASP	LYS	LYS	ALA	GLY
		V699	K646	THR	PRO	ALA	ALA	LYS	GLU	GLY
V772	V772	I700	Q647	PHE	ALA	SER	ASP	PHE	GLY	THR
S773	S773	E701	L648	GLY	PHE	LYS	ASN	SER	ASN	ASN
N774	N774	R702	T649	ALA	SER	PRO	ASN	GLU	ALA	ASN
T775	T775	E650	E650	GLN	PHE	ALA	SER	ASN	ALA	ASN
F776	F776	Q703	S651	LYS	GLY	PHE	ALA	LYS	LYS	ALA
N777	N777	Q704	S651	ASP	ALA	SER	PRO	THR	PRO	ASN
K778	K778	D705	A652	ASN	LYS	PHE	ALA	GLY	LYS	ALA
T779	T779	E706	S653	GLY	ALA	GLY	ALA	GLY	THR	ALA
T780	T780	L707	K654	LYS	GLU	GLY	ALA	PRO	ALA	LYS
N781	N781	E708	H654	THR	GLU	SER	ASN	GLY	LYS	ASN
I782	I782	F655	T659	GLY	LYS	PHE	ALA	LYS	THR	ASN
D783	D783	N709	E656	ASN	ASN	PHE	GLY	LYS	ALA	PHE
I784	I784	D712	Q657	LYS	GLU	ALA	LYS	ALA	SER	GLY
N785	N785	F714	V658	THR	LYS	PHE	ALA	ALA	ALA	LYS
L786	L786	T716	T659	GLY	LYS	GLY	GLY	GLY	LYS	ALA
E787	E787	K717	K659	LYS	LYS	GLY	GLY	GLY	LYS	ALA
D788	D788	E715	K660	SER	LYS	GLY	GLY	PHE	ALA	GLY
		T718	A720	THR	LYS	GLY	GLY	GLY	GLY	GLY
		E719		THR	LYS	GLY	GLY	GLY	GLY	GLY
		K717		THR	LYS	GLY	GLY	GLY	GLY	GLY
		T716		THR	LYS	GLY	GLY	GLY	GLY	GLY
		E715		THR	LYS	GLY	GLY	GLY	GLY	GLY
		F714		THR	LYS	GLY	GLY	GLY	GLY	GLY
		N713		THR	LYS	GLY	GLY	GLY	GLY	GLY
		D712		THR	LYS	GLY	GLY	GLY	GLY	GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	633134	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.483	Depositor
Minimum map value	-1.449	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.18	Depositor
Map size ($\text{\AA}$)	467.59998, 467.59998, 467.59998	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.336, 1.336, 1.336	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.44	1/5810 (0.0%)	0.81	25/7863 (0.3%)
1	M	0.44	1/5787 (0.0%)	0.79	23/7832 (0.3%)
1	N	0.57	0/5852	1.08	26/7931 (0.3%)
1	Z	0.58	0/5853	1.11	35/7931 (0.4%)
2	C	0.75	1/10658 (0.0%)	1.19	10/14443 (0.1%)
2	O	0.75	1/10658 (0.0%)	1.19	12/14443 (0.1%)
3	D	0.48	0/11182	0.83	9/15160 (0.1%)
3	P	0.49	0/11171	0.83	9/15145 (0.1%)
4	E	0.43	1/12583 (0.0%)	0.80	21/17054 (0.1%)
4	Q	0.43	1/12583 (0.0%)	0.79	19/17054 (0.1%)
5	F	0.76	16/12443 (0.1%)	1.57	244/16898 (1.4%)
5	R	0.77	16/12443 (0.1%)	1.57	243/16898 (1.4%)
6	G	0.38	0/1553	0.82	6/2104 (0.3%)
6	J	0.68	0/1509	1.45	35/2042 (1.7%)
6	S	0.38	0/1549	0.83	6/2100 (0.3%)
6	V	0.67	1/1509 (0.1%)	1.42	28/2042 (1.4%)
7	H	0.95	6/1832 (0.3%)	1.35	27/2482 (1.1%)
7	K	0.79	2/1829 (0.1%)	1.51	33/2485 (1.3%)
7	T	0.95	5/1832 (0.3%)	1.35	27/2482 (1.1%)
7	W	0.90	3/1826 (0.2%)	1.74	46/2481 (1.9%)
8	I	0.84	7/1431 (0.5%)	1.35	24/1940 (1.2%)
8	L	0.49	0/1378	1.02	5/1873 (0.3%)
8	U	0.84	6/1431 (0.4%)	1.35	25/1940 (1.3%)
8	X	0.49	0/1378	1.02	7/1873 (0.4%)
All	All	0.62	68/136080 (0.0%)	1.14	945/184496 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	N	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	Z	0	1
5	F	0	4
5	R	0	4
6	G	0	1
6	S	0	1
7	H	0	1
7	K	0	2
7	T	0	1
7	W	0	2
All	All	0	19

The worst 5 of 68 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	427	LEU	C-N	23.26	1.53	1.33
7	T	427	LEU	C-N	23.15	1.53	1.33
5	F	1235	ASN	C-N	14.69	1.53	1.33
5	R	1235	ASN	C-N	14.62	1.53	1.33
7	W	326	LYS	C-N	13.71	1.50	1.33

The worst 5 of 945 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1090	PRO	CA-N-CD	-38.14	58.60	112.00
5	R	1090	PRO	CA-N-CD	-38.10	58.66	112.00
5	F	356	ILE	CA-C-N	20.01	144.86	119.84
5	F	356	ILE	C-N-CA	20.01	144.86	119.84
5	R	356	ILE	CA-C-N	20.00	144.84	119.84

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	1185	ILE	Mainchain
5	F	1188	THR	Mainchain
5	F	360	LEU	Mainchain
5	F	814	ASN	Mainchain
6	G	422	GLY	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5720	0	5578	316	0
1	M	5697	0	5563	313	0
1	N	5766	0	5590	504	0
1	Z	5767	0	5596	531	0
2	C	10452	0	10392	50	0
2	O	10452	0	10392	49	0
3	D	10966	0	10812	464	0
3	P	10956	0	10803	479	0
4	E	12362	0	12566	364	0
4	Q	12362	0	12566	343	0
5	F	12239	0	11567	859	0
5	R	12239	0	11568	867	0
6	G	1533	0	1515	122	0
6	J	1492	0	1465	295	0
6	S	1529	0	1504	111	0
6	V	1492	0	1465	329	0
7	H	1811	0	1697	146	0
7	K	1808	0	1614	314	0
7	T	1811	0	1697	154	0
7	W	1805	0	1605	327	0
8	I	1418	0	1293	172	0
8	L	1366	0	1211	162	0
8	U	1418	0	1293	169	0
8	X	1366	0	1211	142	0
All	All	133827	0	130563	6374	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

The worst 5 of 6374 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:810:ALA:CB	1:N:836:ASP:HA	1.26	1.63
6:G:451:MET:CE	1:M:14:THR:HG21	1.19	1.62
1:A:15:SER:HB2	6:S:447:PHE:CZ	1.35	1.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:955:PRO:CB	3:D:994:SER:CB	1.78	1.61
5:R:1357:ALA:HB2	5:R:1381:LEU:CB	1.19	1.60

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	722/839 (86%)	702 (97%)	18 (2%)	2 (0%)	36	65
1	M	719/839 (86%)	699 (97%)	18 (2%)	2 (0%)	36	65
1	N	736/839 (88%)	680 (92%)	39 (5%)	17 (2%)	5	30
1	Z	736/839 (88%)	681 (92%)	38 (5%)	17 (2%)	5	30
2	C	1323/1391 (95%)	1269 (96%)	41 (3%)	13 (1%)	12	43
2	O	1323/1391 (95%)	1270 (96%)	40 (3%)	13 (1%)	12	43
3	D	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	21	52
3	P	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	21	52
4	E	1538/1655 (93%)	1374 (89%)	150 (10%)	14 (1%)	14	45
4	Q	1538/1655 (93%)	1376 (90%)	149 (10%)	13 (1%)	16	47
5	F	1616/1683 (96%)	1200 (74%)	321 (20%)	95 (6%)	1	15
5	R	1616/1683 (96%)	1196 (74%)	324 (20%)	96 (6%)	1	15
6	G	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	24	56
6	J	191/472 (40%)	172 (90%)	15 (8%)	4 (2%)	5	31
6	S	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	24	56
6	V	191/472 (40%)	171 (90%)	16 (8%)	4 (2%)	5	31
7	H	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	7	34
7	K	252/541 (47%)	208 (82%)	33 (13%)	11 (4%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	T	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	7	34
7	W	252/541 (47%)	209 (83%)	32 (13%)	11 (4%)	2	19
8	I	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1	15
8	L	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	3	25
8	U	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1	15
8	X	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	3	25
All	All	17165/23162 (74%)	15181 (88%)	1612 (9%)	372 (2%)	7	31

5 of 372 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	VAL
2	C	319	PRO
2	C	468	PHE
2	C	476	ASN
2	C	694	PHE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	608/762 (80%)	587 (96%)	21 (4%)	32	54
1	M	605/762 (79%)	581 (96%)	24 (4%)	28	52
1	N	609/762 (80%)	556 (91%)	53 (9%)	9	34
1	Z	609/762 (80%)	555 (91%)	54 (9%)	9	33
2	C	1177/1250 (94%)	1149 (98%)	28 (2%)	43	62
2	O	1177/1250 (94%)	1149 (98%)	28 (2%)	43	62
3	D	1212/1353 (90%)	1198 (99%)	14 (1%)	63	71
3	P	1210/1353 (89%)	1196 (99%)	14 (1%)	63	71
4	E	1421/1557 (91%)	1390 (98%)	31 (2%)	45	63
4	Q	1421/1557 (91%)	1388 (98%)	33 (2%)	44	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	1261/1538 (82%)	1167 (92%)	94 (8%)	12	38
5	R	1261/1538 (82%)	1165 (92%)	96 (8%)	12	38
6	G	167/377 (44%)	162 (97%)	5 (3%)	36	57
6	J	162/377 (43%)	146 (90%)	16 (10%)	7	30
6	S	166/377 (44%)	161 (97%)	5 (3%)	36	57
6	V	162/377 (43%)	147 (91%)	15 (9%)	8	32
7	H	171/439 (39%)	163 (95%)	8 (5%)	23	48
7	K	153/439 (35%)	130 (85%)	23 (15%)	3	16
7	T	171/439 (39%)	163 (95%)	8 (5%)	23	48
7	W	152/439 (35%)	121 (80%)	31 (20%)	1	8
8	I	152/674 (23%)	136 (90%)	16 (10%)	6	28
8	L	138/674 (20%)	136 (99%)	2 (1%)	59	70
8	U	152/674 (23%)	136 (90%)	16 (10%)	6	28
8	X	138/674 (20%)	136 (99%)	2 (1%)	59	70
All	All	14455/20404 (71%)	13818 (96%)	637 (4%)	27	50

5 of 637 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	R	1169	SER
7	W	506	ILE
5	R	1285	HIS
5	R	1167	LYS
8	U	736	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 319 such sidechains are listed below:

Mol	Chain	Res	Type
5	R	154	GLN
7	W	402	GLN
5	R	725	ASN
8	U	695	GLN
1	Z	138	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

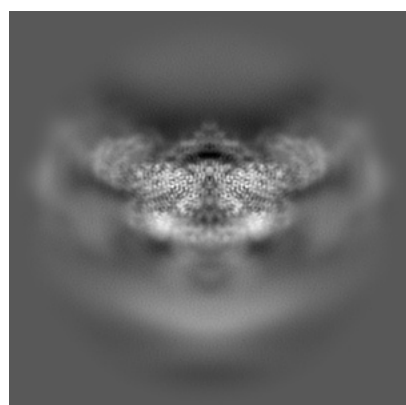
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32658. These allow visual inspection of the internal detail of the map and identification of artifacts.

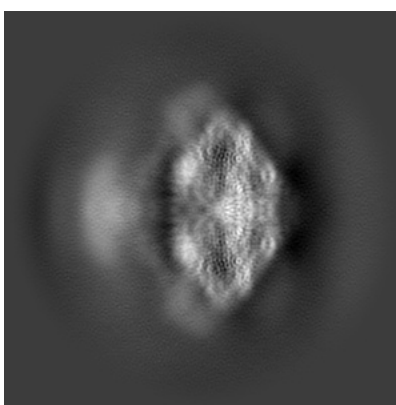
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

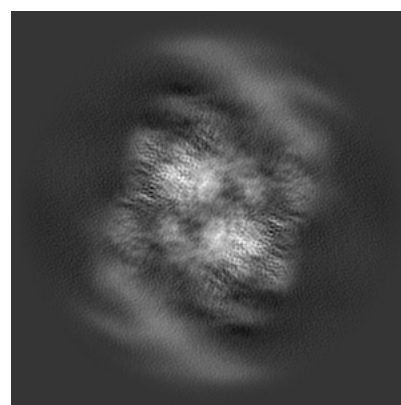
6.1.1 Primary map



X



Y

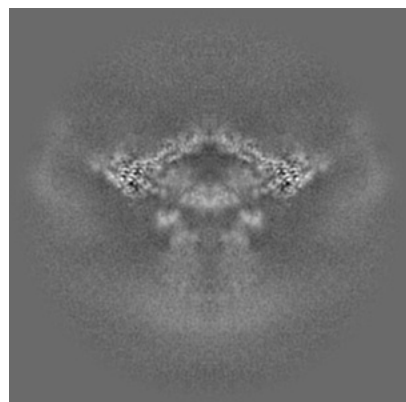


Z

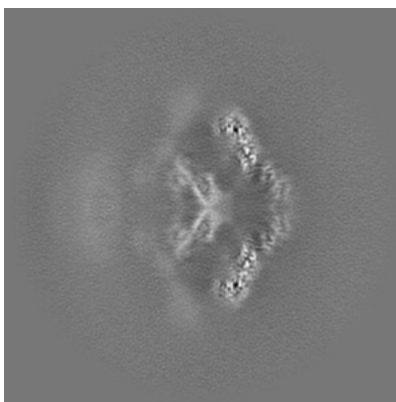
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

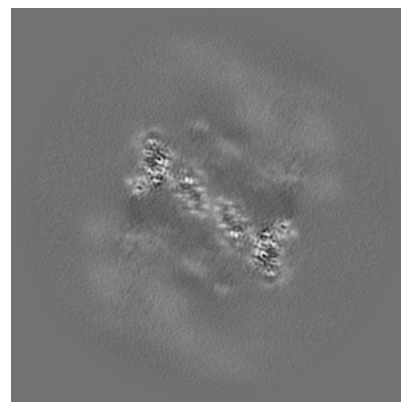
6.2.1 Primary map



X Index: 175



Y Index: 175

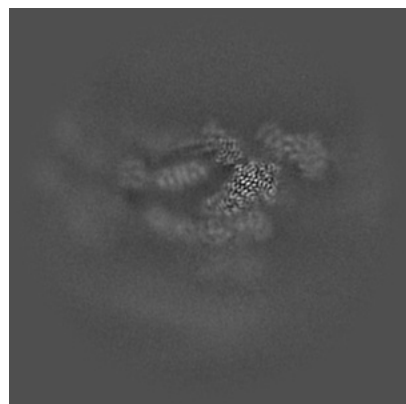


Z Index: 175

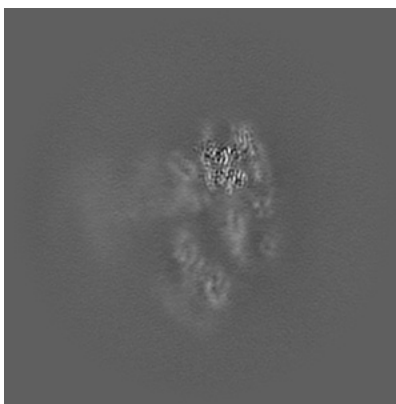
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

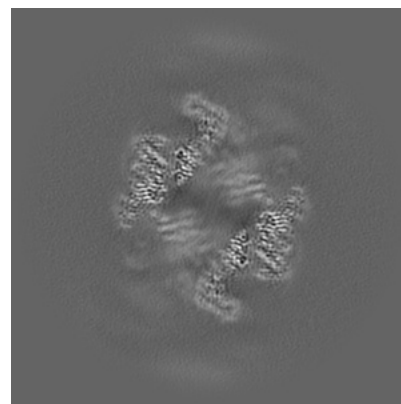
6.3.1 Primary map



X Index: 150



Y Index: 147

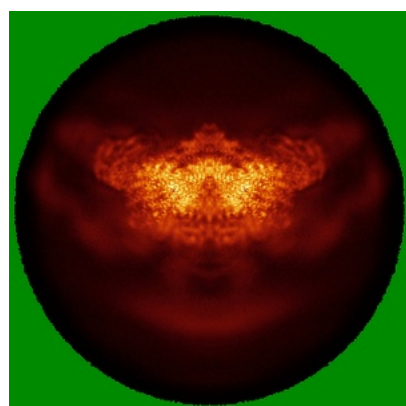


Z Index: 204

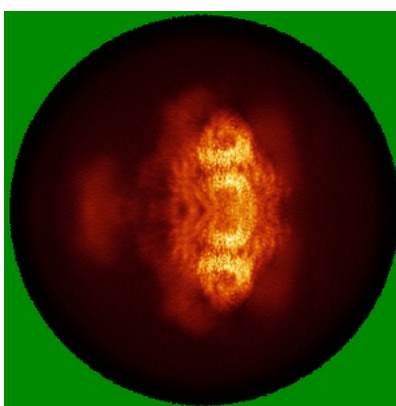
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

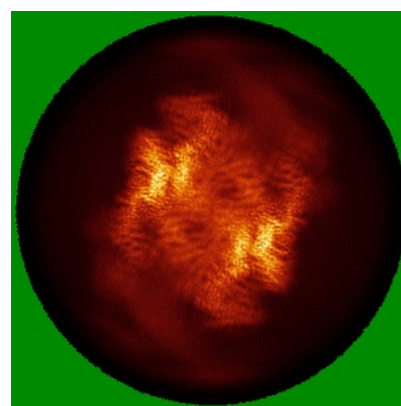
6.4.1 Primary map



X



Y

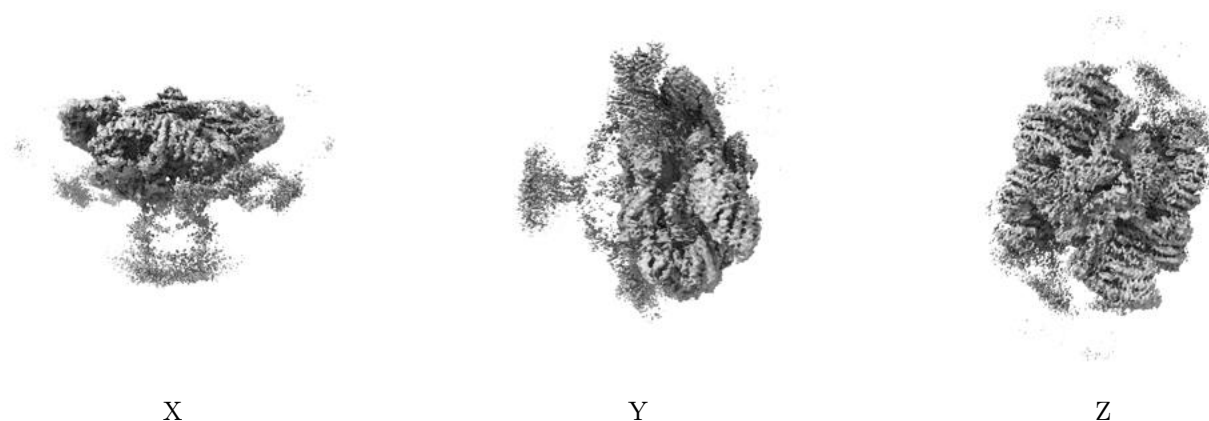


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

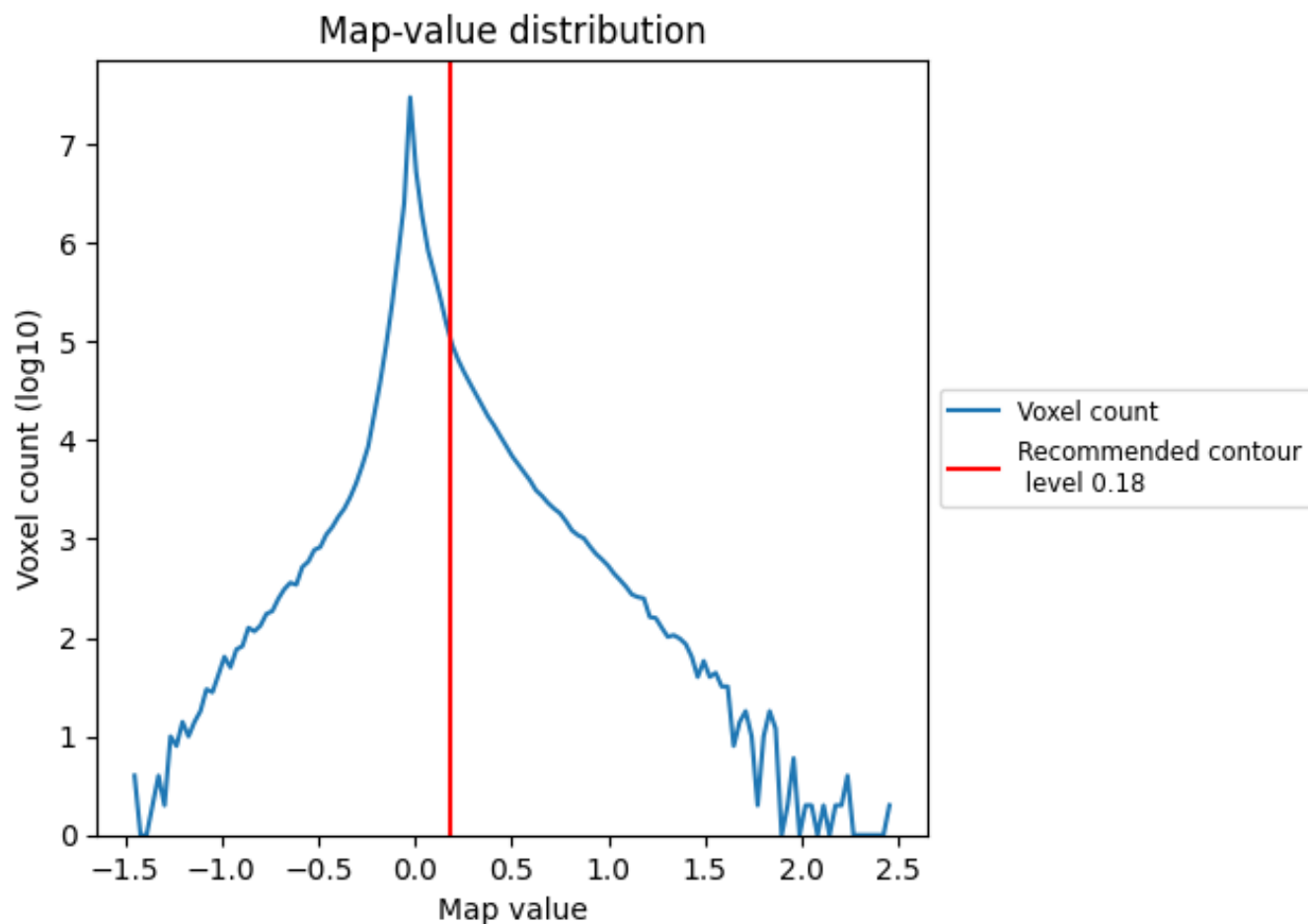
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

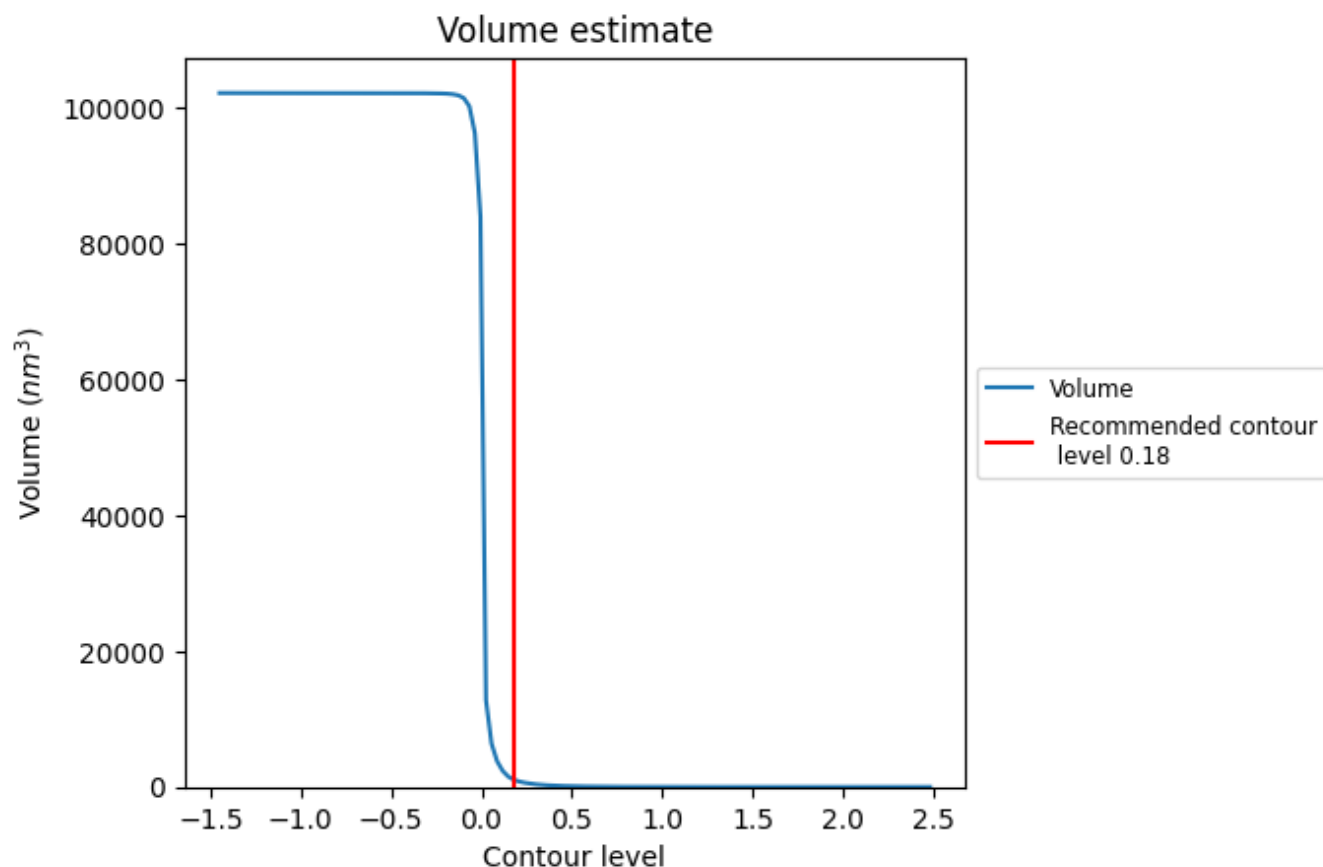
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

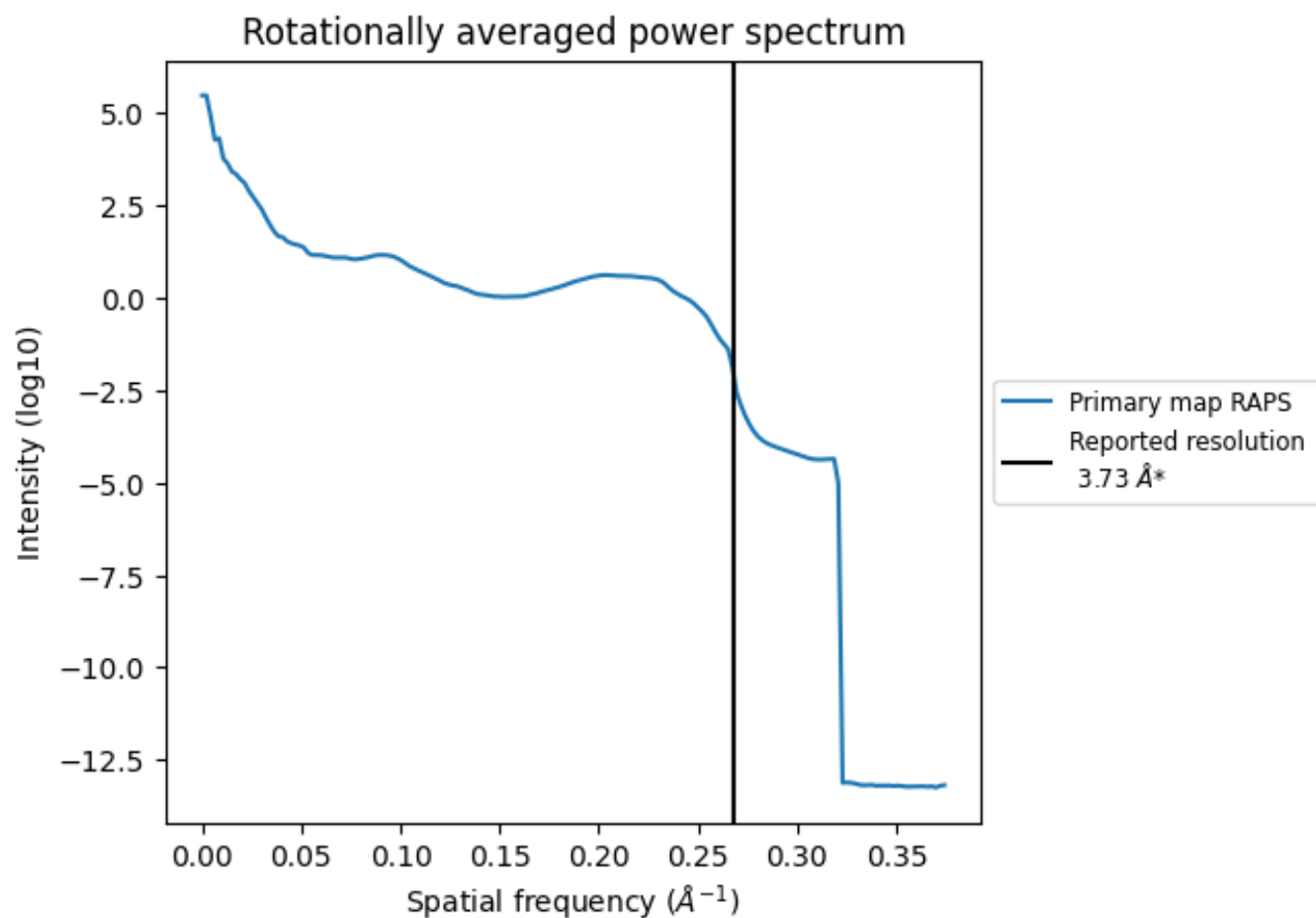
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1052 nm^3 ; this corresponds to an approximate mass of 950 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.268 Å⁻¹

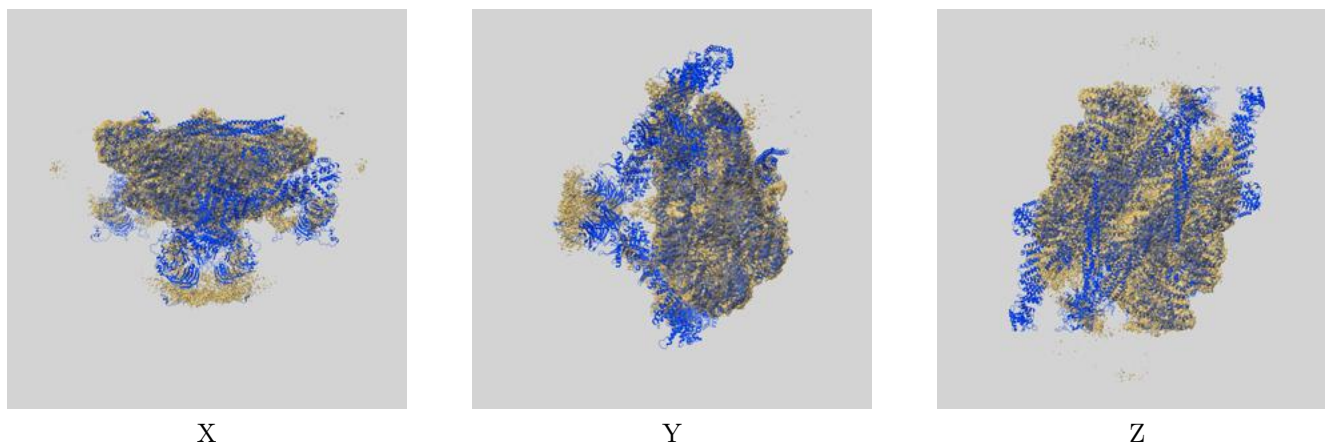
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

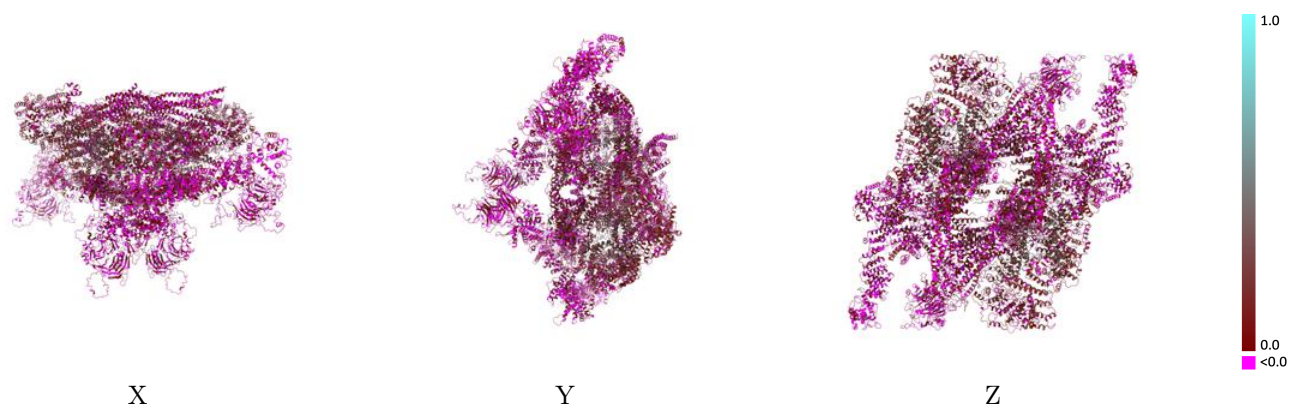
This section contains information regarding the fit between EMDB map EMD-32658 and PDB model 7WOT. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



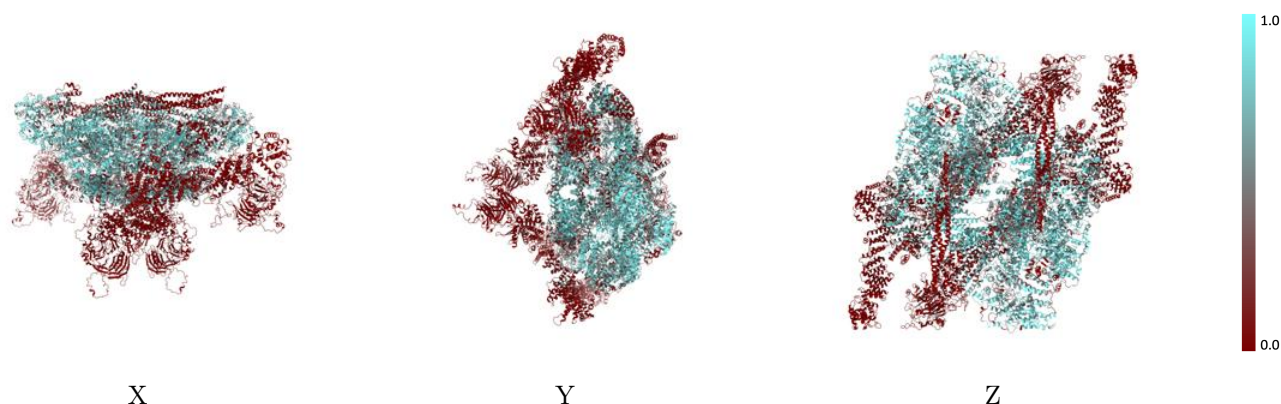
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



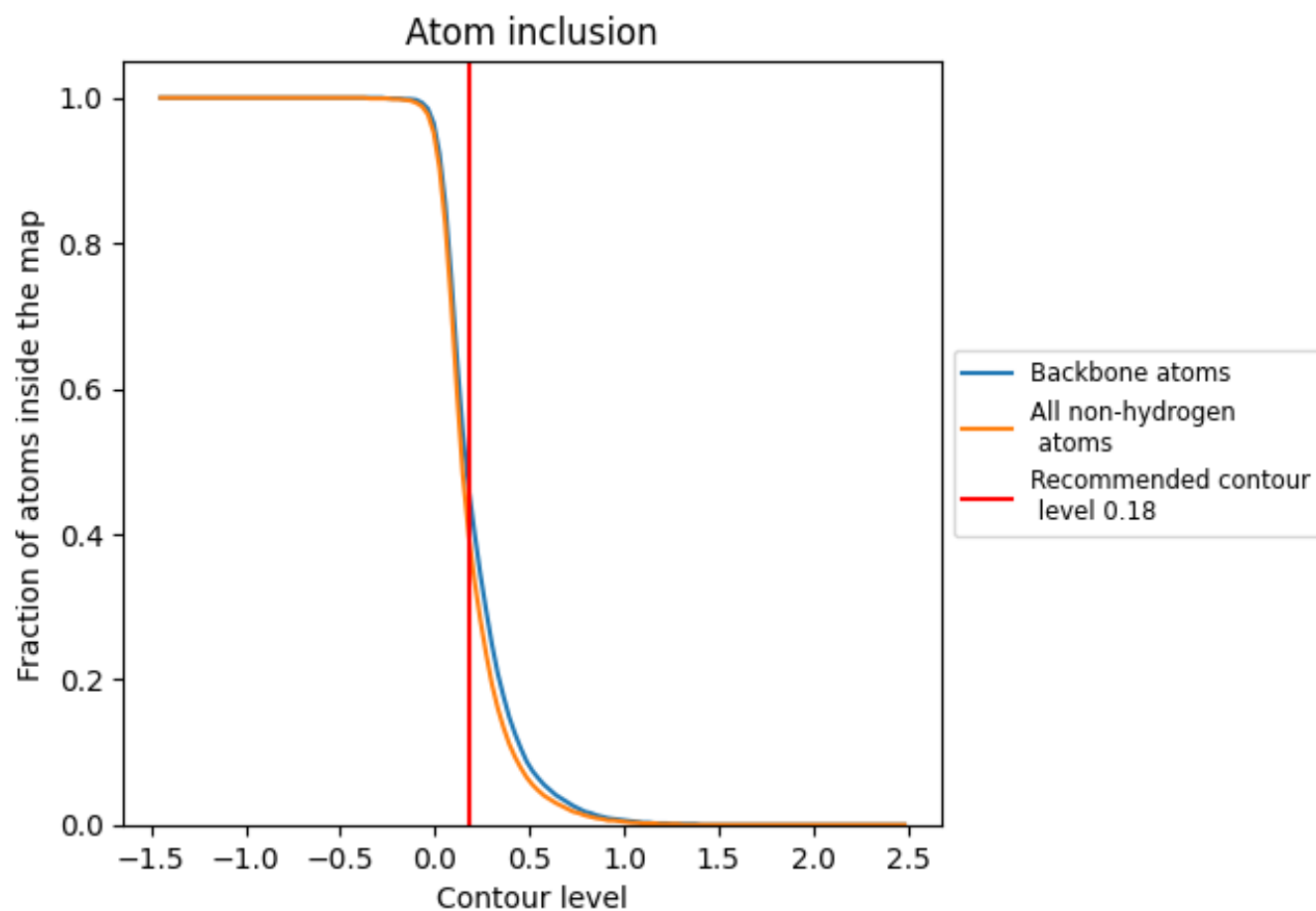
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.18).

9.4 Atom inclusion [i](#)



At the recommended contour level, 46% of all backbone atoms, 40% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3970	 0.0910
A	 0.0870	 -0.0000
C	 0.0190	 0.0100
D	 0.2240	 0.0340
E	 0.6410	 0.1690
F	 0.6670	 0.1830
G	 0.4670	 0.0620
H	 0.4600	 0.0580
I	 0.5910	 0.1040
J	 0.3610	 0.0640
K	 0.2650	 0.0540
L	 0.3360	 0.0640
M	 0.0840	 0.0000
N	 0.5810	 0.1030
O	 0.0190	 0.0090
P	 0.2230	 0.0340
Q	 0.6450	 0.1740
R	 0.6700	 0.1830
S	 0.4670	 0.0620
T	 0.4610	 0.0570
U	 0.5940	 0.1070
V	 0.3640	 0.0620
W	 0.3030	 0.0730
X	 0.3330	 0.0650
Z	 0.5770	 0.1050

